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Sequence:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 90 summaries
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Copyright (c) 1993 - 2002
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-09-352-616A-20
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US-09-371-209-38
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                                                                                                                                          Sequence 20, Appl
Patent No. 5196523
Sequence 23, Appl
Sequence 372, App
Patent No. 5196523
Patent No. 5196523
Patent No. 5196523
Sequence 15, Appl
Sequence 123, Appl
Sequence 20, Appl
Sequence 30, Appl
Sequence 31, Appl
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Sequence
                 20, Appl
38, Appl
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equence 7,	equence 7,	equence 10	equence 8,	equence 12,	equence 7,	equence 12,	equence 43,	equence 1,	equence 1,	equence 15	equence 1,	equence 1,	equence 7,	equence 29,	equence 65,	equence 1,	equence 7,	equence 7,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1	equence 10	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	equence 1,	• •	cent No. 5	equence 1,	tent No. 5	equence 25	equence 25,	uence 25,	equence 9,	equence 31,	equence 7
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ALIGNMENTS

RESULT 1

US-08-248-474-36

V; Sequence 36, Application US/08248474

; Patent No. 5612471
; GENERAL INFORMATION:

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RESULT 2
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                                                                                                                                                                                                                                                                                                                  Sequence 36, Applic
Patent No. 6093810
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                           APPLICANT: Bird, David McK APPLICANT: Wilson, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
NUMBER OF SEQUENCES: 114
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                                                                                                                                STREET: 'Two L....
CITY: San Francisco
CITY: 7-1:fornia
                                                                                                                                                   ADDRESSEE: Townsena and townsena Eighth Floor
         SOFTWARE:
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OTHER INFORMATION: /standard_name= "DB# 155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                           97 CCAATATTATTTACCACG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 25-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCAATNNNNNNNNNCCACG 19
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Bastian, Kevin L.
34,774
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                                                                                                                                                                                                                                                                                                                                   Application US/08756849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                Bird, David McK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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                                                                                                                     USA
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         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                       Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum cv 'Rutgers Large
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52.6%;
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Pred. No.
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. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5849491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20,
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                                                                                                                                                                        ZIP: 10598-441.

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKette, 3.5 inch, 1.44 Mb

COMPUTER: IBM Compatible

COMPUTER: OF 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004,157
FILING DATE: 20-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yap, Wai HO
TITLE OF INVENTION: MET
TITLE OF INVENTION: SEC
TITLE OF INVENTION: COM
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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LENGTH: 272 base pairs
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                            STREET: 1992 CONTROL OF STREET: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 CCAATATTATTTTACCACG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 1..272
OTHER INFORMATION: /sta
                                                                                                             FILING DATE:
                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08716942
                                                                                                                                                                                                                                                                                                                          E: Oppedahl & Larson
1992 Commerce Street, Suite 309
                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                  Word Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warren, R. Antony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radomski, Christopher C. A. Seow, Kah Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terragen Diversity Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum cv 'Rutgers Large Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                  METHOD FOR ISOLATING XYLANASE GENE SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD COMPOSITIONS OBTAINED THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "DB# 155
                                                                                                                              US/08/716,942
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Pred. No. 3.6e+02;
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Gaps

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RESULT 5
5196523-1
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US-09-130-337A-20/c
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                                                                                                                                                                                                                                          US-09-130-337A-20
; Patent No. 5196523 ...
; APPLICANT: LEE, AMY S.
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Best Local
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                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Warren, RAJ
APPLICANT: Yap, WH
TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIC
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 9993-004
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/130,337A CURRENT FILING DATE: 1998-08-06 PRIOR APPLICATION NUMBER: 08/716,942 PRIOR FILING DATE: 1996-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/004,157 PRIOR FILING DATE: 1995-09-22
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                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Unknown organism
                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of unknown organism:
                                                                                                                                                                                                                                                                                                                             LENGTH: 296
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: no FRAGMENT TYPE: internal ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 CCAATGGTTGTGGCCCACG 199
                                                                                                   217 CCAATGGTTGTGGCCCACG 199
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                                                                                                                                      1 CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                       Local Similarity
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52.6%;
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                                                                                                                                                             Score 10; DB 4; pred. No. 3.7e+02; Indels
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Pred. No. 3.7e+02;
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                                                                                                                                                                                                       Length 296;
                                                                                                                                                                                                                                                              soil microbe
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RESULT 6
US-08-804-372A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5196523-1
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                                                                US-08-804-372A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08804372A Patent No. 6183753
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               Query Match
Best Local Similarity
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APPLICANT: Cochra
                                                                                                                                                                                                           TELEFAX: (212) 391-05: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-MAY-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wild, Martha A. APPLICANT: Winslow, Barbara J. TITLE OF INVENTION: Recombinan TITLE OF INVENTION: Thereof
                                                                            MOLECULE N
HYPOTHETICAL: N
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 CCAATCGGAGGCCTCCACG 300
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                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 282,880
                                                                                                                                                                                                                                                                          NAME: White, John P.
REGISTRATION NUMBER: 28.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/804,372A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New Yor
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                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                              (212) 391-0525
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   Conservative
                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cooper & Dunham LLP
                                                                                                                                                                                                                                            (212) 278-0400
                                                                                                NO
                                                                                                            DNA (genomic)
                                                                                                                                              double
               52.6%;
52.6%;
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52.6%;
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Pred. No. 3.8e+02;
   0;
                  Score 10; DB 4;
Pred. No. 3.9e+02
                                                                                                                                                                                                                                                                            2552/39115E
 Mismatches
                                 DB 4;
   9;
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   Indels
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Gaps
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Matches

1 CCAATNUNNNNNNCCACG 19

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5196523-22
; PATENT NO. 5196523
; PATENT NO. 5196523
TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE, CALCIUM AND TEMPERATURE
NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
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                                                                                                                                                                       RESULT 9
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: Sequence 372, Application US/09404879A

: Patent No. 6468546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LEE, AMY S.
TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE, CALCIUM AND TEMPERATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-JAN-1985
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Best Local :
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 282,880
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 690,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                        311 CCAATCGGAGGCCTCCACG 329
FILING DATE: 19-MAY-1989
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/(FILING DATE: 19-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 CCAATCAAAAGCTGCCACG 280
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 CCAATCCAGGAGGTCCACG 19
                                                                                                                                                                                                                                                             1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                   52.6%;
52.6%;
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52.6%;
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               US/07/354,988
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/ Pred. No. 3.9e+02;
/ Thos 9;
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                   Score 10; DB 6;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                DB 6; Length 399;
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XRESULT 10
US-08-609-657-15
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US-08-609-657-15
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                                                                    Matches
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Patent No. 5681706
                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                              TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-POS/ microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01 March 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 282,880
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 690,951
FILING DATE: 01-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stoler, Daniel L.
TITLE OF INVENTION: Mammalian Anoxia-Responsive Regulatory
TITLE OF INVENTION: Element
361 CCAATTGTATGTAACCACG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 CCAATCGGCGGCCTCCACG 329
                                                                Local Similarity
nes 10; Conserv
                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                    NAME: Nelson, M. Bud REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/609,657 FILING DATE: 01 March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1800 C
                                 1 CCAATUNNUNUNUCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 421
                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                424 nucleotides
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                                                                  Conservative
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                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hodgson, Russ, Andrews, Woods & Goodyear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette, 3.5 inch
                                                                                                                                                                                               single-stranded
                                                                                52.6%;
52.6%;
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52.6%; Pred. No. 3.9e+02;
"Mismatches 9;
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                                                           Score 10; DB 1; Le
Pred. No. 3.9e+02;
0; Mismatches 9;
                                                                                              Length 424;
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RESULT 11 US-09-257-584-8/c ; Sequence 8, Application US/09257584A

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US-09-257-584-8
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US-09-222-575-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6177611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 123, Application US/09222575
Patent No. 6387697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/257,584A CURRENT FILING DATE: 1999-02-25 EARLIER APPLICATION NUMBER: 60/076,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rice, Douglas A.
TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 5718-33, 035718/175218
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Jiangchun TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer TITLE OF INVENTION: and Methods for Their Use FILE REFERENCE: 210121.470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Dav
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/222,575
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Nucleotide at this postion may be a or g or c or OTHER INFORMATION: t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: cab-10 promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 467
                                                                                                                                                                                                                                 NAME/KEY: modified_base
LOCATION: (152)
OTHER INFORMATION: where n is
NAME/KEY: modified_base
LOCATION: (373)
             OTHER INFORMATION: Where n is NAME/KEY: modified_base LOCATION: (502)
                                                                                                                                        OTHER INFORMATION: Where NAME/KEY: modified_base
                                                                                                                                                                                                                  LOCATION: (373)
OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
OTHER INFORMATION: Where n is a, c,
                                                                      NAME/KEY: modified_base LOCATION: (496)
                                                                                                        OTHER INFORMATION: Where n
                                                                                                                                                                                LOCATION:
                                                                                                                                                                                               NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 531
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Mitcham, Jennifer L.
                                                                                                                             (494)
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52.6%;
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Pred. No.
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                                                                                                                     'RESULT 14
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                                                                 , Sequence 20, Application US/09030607
; Patent No. 6262245
                                                                                                     US-09-030-607-20
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                                                                                                                                                                                                                                                                                                           US-09-020-956-20
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Patent No. 6261562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 52.6%;
Best Local Similarity 52.6%;
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                                                                                                                                                                                                                                     Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Jiangchun APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 CCAATTTTCAAGCACCACG 524
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                       303 CCAATTGTTTTTNGCCACG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 09-FE
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                             754 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                                                            single
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Pred. No. 4.1e+02;
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                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                         Score 10; DB 4;
Pred. No. 4.3e+02;
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                                                                                                                                                                                                                                              Mismatches
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CORRESPONDENCE ADDRESS

STREET: ADDRESSEE:

6300 Columbia Center, 701 Fifth Avenue

SEED and BERRY LLP

Seattle

NUMBER OF SEQUENCES:

COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS

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RESULT 15
US-09-605-785-20
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                                                                              APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMMOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
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LOCATION: (1)...(754)
              NAME/KEY: misc_feature
                                  ORGANISM: Homo sapien FEATURE:
                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: sing TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 25-FEE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                         Li, Samuel
                                                                                                                                                                                                                                                                                                                     Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                         Day, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                      Fanger, Gary R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Susan L.
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APPLICANT: SOIK, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 754
TYPE: DNA
ORGANISM: Homo sapien
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US-09-352-616A-20
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SEQ ID NO 20
LENGTH: 754
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Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
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                                                                                     APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Jennifer Lynn TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE FILE REPERENCE: 210121.427C8
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APPLICANT:
APPLICANT:
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                                               CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Local Similarity 57.9%;
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                              FastSEQ for Windows Version 3.0
                                                                                                                                                                      Jiang, Yuqui
Xu, Jiangchun
                                                                                                                                                                                                             Harlocker, Susan Louise
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Reed, Steven G.
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57.9%;
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Pred. No. 4.3e+02;
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Pred. No. 4.3e+02;
"'-matches 8; Indels
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NAME/KEY: misc_feature

; LOCATION: (1)...(754)

; OTHER INFORMATION: n = A,T,C or G

US-09-352-616A-20
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US-09-232-149A-20
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; LCCATION: (1)...(754)
; OTHER INFORMATION: n - A,T,C or G
US-09-232-149A-20
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US-09-171-209-38
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CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
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                                                                                                                                                                                                                                                                                                                               Sequence 38, Application US/09171209
Patent No. 6448000
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapien
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ZIP: 30303-1811
COMPUTER READABLE FORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 83
                                                                                                                                                                                                                                   TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL INFECTION
                                                                                                                                                                                                                                                                                                                 APPLICANT: VANDERBILT UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                       ADDRESSEE: Needle & Rosenberg, P.C. STREET: 127 Peachtree Street, Suite 1200
                                                                               COUNTRY: USA
ZIP: 30303-1811
                                                                                                                  CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                              Nashville, TN 37240
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57.9%;
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Pred. No. 4.3e+02;
"'-matches 8;
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Pred. No. 4.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 754;
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                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: CH 0016/97
FILING DATE: 31 DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meiss, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
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                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/998,416 FILLING DATE: 24-DEC-1997
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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REFERENCE/DOCKET NUMBER: PF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 52.6%; Score 10; DB 4; Length 843; Local Similarity 52.6%; Pred. No. 4.4e+02; hes 10; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U:
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 404 688 0770
TELEFAX: 404 688 9880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Selby, Elizabeth REGISTRATION NUMBER: 38,298 REFERENCE/DOCKET NUMBER: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US97/06067 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08998416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
REVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 6239264artis Corporation
                         PF/5-30306/A/CGC1976
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US-09-137-855-1/c
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US-09-541-941B-21/c
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SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 904
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09137855B Patent No. 6242237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Wang, Jun
APPLICANT: Shaw, Pang Chui
        EARLIER APPLICATION NUMBER: 0233/96
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: 0235/96
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: PCT/DK97/00092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                  APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Andersen, Lene N.
APPLICANT: clausen, Ib G.
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: An Enzyme With Galactanase Activity
FILE REFERENCE: 4886.204-US
  EARLIER |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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                                                                                                                    CURRENT APPLICATION NUMBER: US/09/137,855B
CURRENT FILING DATE: 1998-08-21
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Best Local
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APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
TITLE OF INVENTION: FOR THE AUTHENTICATION OF HERBAL CHINESE MEDICINES
TILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/541,941B
CURRENT FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Campanumoea Javanica Blume
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: USEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              646 CCAATATCCGCTTCCCACG 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.6%;
Local Similarity 52.6%;
es 10; Conservation
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STRANDEDNESS: single
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1997-02-28
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; TYPE: DNA
; ORGANISM: Myceliophthora thermophila
US-09-137-855-1
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LENGTH: 1117
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rafalski, J. Antoni
APPLICANT: Falco, S. Carl
TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
FILE REFERENCE: BB-1174-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09347819 Patent No. 6184036
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EARLIER FILING DATE: July 17, 1998
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/347,819
CURRENT FILING DATE: 1999-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Office 97
NAME/KEY: unsure
LOCATION: (1100)
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                                                                          FEATURE:
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LOCATION: (227)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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(1043)
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; FEATURE:

NAME/KEY: misc_feature

LOCATION: (100)..(100)

OTHER INFORMATION: n = a, t, c, g, or u
US-09-541-941B-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                           SEQ ID NO 27
                                                                                                                                                                                                                                 APPLICANT: Wang, Jun
APPLICANT: Shaw, Pang Chui
APPLICANT: Shaw, Pang Chui
APPLICANT: Paul, Pui-Hay
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
TITLE OF INVENTION: POR THE AUTHENTICATION OF HERBAL CHINESE MEDICINES
FILE REFERENCE: 2913/52188-ZA
CURRENT APPLICATION NUMBER: US/09/541,941B
CURRENT FILING DATE: 2000-04-03
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                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 1137
                                                                                                           TYPE: DNA ORGANISM: Pheretima Aspergillus
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                                                                                                                                                    LENGTH:
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                                                                                                                                                      1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%; Score 10; DB 4; 52.6%; Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.6%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1117;
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                                                                            TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-OCT-
PRIOR APPLICATION DATA:
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                  FEATURE
                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-1005
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 28-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/OFILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                         FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/FR/91/00855 FILING DATE: 29-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                     TOPOLOGY:
                                                                   STRANDEDNESS:
NAME/KEY: CDS
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SYSTEM: PC-DOS/MS-DOS
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                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-1992
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                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                           31-OCT-1990
                                                                     unknown
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52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
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 Mismatches

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Pred. No. 4.7e+02;
                                                                                                                                                                                                                               660-060-0 PCT
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US-08-286-819A-31
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                                                                                                 NFORMATION FOR SEQ ID NO:
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     MOLECULE TYPE:
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                    FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
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APPLICANT:
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                                   STRANDEDNESS:
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                                                                     LENGTH:
                                                                                                                                     TELEFAX:
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                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 9013579
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/917,146 FILING DATE: 10-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 05-AUG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                : (703) 413-2220
248855 OPAT UR
                                                              1347 base pairs
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                     linear
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                                                eic acid
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                                                                                                                                                   (703) 413-3000
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DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1994
                                 unknown
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                                                                                                                                                                                  660-060-0 PCT
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Pred. No. 4.8e+02;
0; Mismatches 9
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US-08-980-357-7
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                                                                                                                        TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                   FEATURE:
                                 MOLECULE TYPE:
                                                                                                                                                                                                                                         APPLICATION NUMBER: FR 90 FILING DATE: 31-OCT-1990 ATTORNEY/AGENT INFORMATION.
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: [10-AUG-:
PRIOR APPLICATION DATA:
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PRICE APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUREENT APPLICATION DATA:
AFPLICATION NUMBER: US/08/980,357
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: ECORRESPONDENCE ADDRESS:
NAME/KEY: CDS
                                                 TOPOLOGY:
                                                             STRANDEDNESS:
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                                                                                                                                                                                                                  NAME: Oblon, No. 60 REGISTRATION NUMBER:
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                                                                                            LENGTH:
                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 29-007
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-AUGAPPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 01
FILING DATE: 05-AUG-1994
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                                                                        nucleic acid
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Y: U.S.A.
                                                                                      1347 base pairs
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1755 S. Jefferson Davis Highway, Suite 400
                                              unknown
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MOLINAS, CATHERINE
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                            DNA (genomic)
                                                             unknown
                                                                                                                                                                                                                                                                                                                                                         UMBER: US 07/917,146
10-AUG-1992
                                                                                                                                                                                                                                                                                                             29-OCT-1991
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28-DEC-1993
                                                                                                                                                    413-2220
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; MOLECULE TYPE: US-08-980-357-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOLINAS, APPLICANT: COURVALIN TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                  TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 01 FILING DATE: 28-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                              FILING DATE: 31-OCT-1990
ATTORNBY/AGENT INFORMATION:
ANAME: Oblon, NO. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/980,357 FILING DATE:
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                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FR 90
FILING DATE: 31-OCT-1990
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/917,146 FILING DATE: 10-AUG-1992
                                                                                                                                                                              TELEPHONE:
                                     TOPOLOGY:
                                                      STRANDEDNESS:
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1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                                                                             (703) 413-3000
(703) 413-2220
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                                       linear
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IUMBER: US 08/174,682
                  DNA (genomic)
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Pred. No. 4.7 indels
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                                                                                                                                                                                                                     ORGANISM: Staphylococcus epidermidis US-09-134-001C-1389
                                                                         Вþ
                 Search completed: November 16, 2002, 03:33:38
Job time : 50 secs
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Best Local Similarity
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                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                        LENGTH: 1377
TYPE: DNA
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SUMMARIES

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                   E28797 19 bp DNA linear PAT 1 Endoplasmic reticulum stress-response regulatory element. E28797 E28797.1 GI:13020851 JP 1999243959-A/1.
     unidentified.
unidentified
unclassified
                                                                                                                      19;
                                                                                                                                                                                                  Patent: WO 0171018-A 1 27-SEP-2001;
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)
                                                                                                                                                                                                                    transfer
                                                                                                                                                                                                                       Secreting products from skin by adeno-associated virus (aav) gene
                                                                                                                                                                                                                                 Hermonat, P.L., Mane, M. and Liu, Y.
                                                                                                                                                                                                                                                 unclassified
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E Hideo, Y., Hideki, Y. and Takashi, Y.

E Hideo, Y., Hideki, Y. and Takashi, Y.

E Endoplasmic reticulum stress-response regulatory element

Patent: JP 199243959-A 1 14-SEP-1999;

HSP RESEARCH INST INC

OS Unidentified
PN JP 199243959-A/1
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00,C12N1
PC A61K37/02
CC Strandedness: Double;
FH Key
FT enhancer 1..19.
      10; Conservative
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JP 1999243959-A/5.
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E28801
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
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/db_xref="taxon:9606"
9 c 5 g
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5 c 1 g
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1.8e+04;
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TITLE
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Endoplasmic reticulum stress-response regulatory element
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Patent: JP 1999243959-A 6 14-SEP-1999;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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   PC PC
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JP 1999243959-A/7.
Rattus sp.
                                                                                                                                                                                                                                                                                                             Endoplasmic reticulum stress-response regulatory element
                                                                                                                                                               Hideo, Y., Hideki, Y. and Takashi, Y.
                                                                                                                                                                                             Rattus
                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                       Rattus sp.
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JP 1999243959-A/6
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C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
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HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
                                                           04-MAR-1998 JP 1998052453
                                                                                         Rattus sp. (rat)
JP 1999243959-A/7
                                                                            14-SEP-1999
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8 c 5 q
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52.6%;
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Pred. No. 1.8e+04;
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RESULT 6
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E28805
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Local Similarity 52.6%;
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OS Homo sapiens (human)
PN JP 1999243959-A/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endoplasmic reticulum stress-response regulatory element Patent: JP 1999243959-A 8 14-SEP-1999;
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Gallus sp.
Gallus sp.
                                                                                                                                                                                    10;
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                                                          Endoplasmic reticulum stress-response regulatory element
                         JP 1999243959-A/9.
                                                                        E28805
                                    E28805.1 GI:13020859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 19)
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
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                                                                                                                                                                                                                                                                                                                                   Topology: Linear;
                                                                                                                                                                                                                                                                                                                                                 Strandedness: Double;
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/db_xref="taxon:10118"
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                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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Pred. No. 1.8e+04;
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                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19)
Hideo, V., Hideki, V. and Takashi, Y. Endoplasmic reticulum stress-response regulatory element Patent: JP 199243959-A 10 14-SEP-1999;
HSP RESEARCH INST INC
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                       HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
                                                                                                                              ennancer
                                                                                                                                                       Topology: Linear;
                                                                                                                                                                  Strandedness: Double;
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                                                                                                                                                                                                                                     04-MAR-1998 JP 1998052453
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                                                                                                                                                                                                                                                               Homo sapiens (human) JP 1999243959-A/10
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                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                             Location/Qualifiers
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/db_xref="taxon:9036"
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  Pred. No.
             Score 10;
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Pred. No. 1.8e+04;
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TITLE
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                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19)
Hideo, Y., Hideki, Y. and Takashi, Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 12 14-SEP-1999;
PD
PF
PR
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                                                                                                                                                         Homo sapiens
                                                                                                                                                                                 E28808.1 GI:130208
JP 1999243959-A/12.
                                                                                                                                                                                                                    Endoplasmic reticulum stress-response regulatory element
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Gallus sp.
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                                                             RESEARCH INST INC
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     04-MAR-1998 JP 1998052453
                                  Homo sapiens (human)
JP 1999243959-A/12
                   14-SEP-1999
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
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JP 1999243959-A/11
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                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gallus sp.
/db_xref="taxon:9036"
9 c 5 g
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Pred. No. 1.8e+04;
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E28809
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Best Local Similarity
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                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
Hidee, Y., Hideki, Y. and Takashi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E28809
E28809.1 GI:13020863
Endoplasmic reticulum stress transcription factor. E44202 E44202.1 GI:18633455
                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 13 14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endoplasmic reticulum stress-response regulatory element.
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                                      E44202
                                                                                                                                                                 Similarity
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Mus sp. (mouse)
JP 1999243959-A/13
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                                                                                                                                                                                                                                                                                                                    Strandedness: Double;
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
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04-MAR-1998 JP 1998052453
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/db_xref="taxon:9606"
6 c 5 g
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6 c 6 g
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Pred. No. 1.8e+04
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                                                                                         TAKASHI YURA
PC C12N15/00, PC
(C12N15/00, PC
CC
FH Key
FT Source
FT
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CC
CC
EH Key Location/Qualifiers
FT source 1 19
/organism='Artificial Sequence'.
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Patent: JP 2001054391-A 5 27-FEB-2001;
HSP RESEARCH INST INC
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19)
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JP 2001054391-A/5.
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Patent: JP 2001054391-A 1 27-FEB-2001;
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Endoplasmic reticulum stress transcription factor
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1 (bases 1 to 19)
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                                                                                                                                                                                                                                                           Homo sapiens (human)
JP 2001054391-A/5
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            /organism="Homo sapiens"
/db_xref="taxon:9606"
9 c 5 g
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5 c 1 g
                                                                       /organism='Homo sapiens (human)'
Location/Qualifiers
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TITLE
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Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T Endoplasmic reticulum stress transcription factor Patent: JP 2001054391-A 7 27-FEB-2001; HSP RESEARCH INST INC OS Rattus sp. (rat)
                                                                                                                                     Rattus sp. Rattus sp.
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HSP RESEARCH INST INC
OS Mus sp. (murine)
PN JP 2001054391-A/6
DD 27-FEB-2001
PD 27-FEB-2001
PF I1-NOV-1999 JP 199321743
PR KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HII
                                                                                                                                                                  Endoplasmic reticulum stress transcription E44208 E44208.1 GI:18633461 JP 2001054391-A/7.
                                                                                         Rattus
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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PC C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00
(C12N15/00, PC C12R1:91)
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E44207.1 GI:18633460
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Endoplasmic reticulum stress
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Pred. No. 1.8e+04;
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Pred. No. 1.8e+04;
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mes 10; Conserv
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CCAATCGCGCCGCACCACG 19
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PC C12N15/09,(C12N15/00, PC
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FH Key
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OS
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HSP RESEARCH INST INC
OS Homo sapiens (human)
PN JP 2001054391-A/8
PD 27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

1 (bases 1 to 19)

Haji, K., Yoshida, H., Mori, K., Yanagi, H. and Yura, T.

Endoplasmic reticulum stress transcription factor

Endoplasmic reticulum stress and transcription factor
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N15/00, PC C12R1:91)
                                                       Conservative
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27-FEB-2001
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/db_xref="taxon:9606"
10 c 4 g
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Location/Qualifiers
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Pred. No. 1.8e+04,
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TAKASHI YURA
PC C12N15/0
(C12N15/00, P
CC
CC Key
                                                           Patent:
HSP RESE
OS HOM
PN JP
PD 27
PF 11
PR KY
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E44211.1 GI:18633464
JP 2001054391-A/10.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                 Haji.K., Yoshida,H., Mori.K., Yanagi,H. and Yura,T. Endoplasmic reticulum stress transcription factor Patent: JP 2001054391-A 10 27-FEB-2001; HSP RESEARCH INST INC
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 19)
                                                                                                                                                                                                                                                                                 Endoplasmic reticulum stress transcription
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                     Homo sapiens.
                         C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00N15/00, PC C12R1:91)
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N15/00, PC C12R1:91)
                                                           KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI,
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                                                                                                            JP 2001054391-A/10
                                                                                                                       Homo sapiens (human)
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                                                                                                27-FEB-2001
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/db_xref="taxon:9036"
7 c 6 g
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transcription factor.
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1.8e+04;
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PC C12N15/0
(C12N15/00, P
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E44213.1 GI:18633466
JP 2001054391-A/12.
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Endoplasmic reticulum stress transcription
Patent: JP 2001054391-A 11 27-FEB-2001;
HSP RESEARCH INST INC
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Endoplasmic reticulum
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/db_xref="taxon:9606"
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52.6%;
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Pred. No.
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                                                      bp DNA
transcription
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1.8e+04;
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Homo sapiens

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                                                                                                                                      PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YA
TAKASHI YURA
PC C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00
(C12N15/00, PC C12R1:91)
CC C12R1:91)
FH Key Location/Qualifiers
FH source 1.19
FT /organism='Mus sp. (murine)'.
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PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
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Endoplasmic reticulum stress transcription factor
Patent: JP 2001054391-A 12 27-FEB-2001;
HSP RESEARCH INST INC
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Mammalia; E
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JP 2001054391-A/13
27-FEB-2001
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JP 2001054391-A/12
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                                             /organism="Mus sp."
/db_xref="taxon:10095"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                     synthetic construct
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AX447733
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/db.xref="taxon:32630"
/note="Computer Generated Probe Sequence."
5 c 9 g 7 t
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/db_xref="taxon:32650"
/note="Computer Generated Probe Sequence."
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HSP RESEARCH INST INC
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1 (bases 1 to 29)
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                                                                                                                                                                                                                                                                                                                                                                        Human alpha-1(III) collagen gene, exon 22.
M10797
                                                                                                                                                                                                                                                                                                                                            alpha-1 type III collagen.
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                                                                                                                                                              J. Biol. Chem. 260 (7), 4357-4363 (1985) 85157600
                                                                                                                                                                                                      Chu,M.L., Weil,D., de Wet,W., Bernard,M., Sippola,M. and Ramirez,F. Isolation of cDNA and genomic clones encoding human pro-alpha 1 (III) collagen. Partial characterization of the 3' end region of
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                  Homo sapiens
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/codon_start=1
               /note="exon 22"
                               /gene="COL3A1"
                                                            /tissue_lib="of
                                                                                       /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10; DB 6;
Pred. No. 1.8e+04;
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                                                              A.Bank and T.Maniatis"
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BASE COUNT
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Best Local Similarity 52.6%;
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                                             DEFINITION
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                                                                                                            AX343726
                                                                                                                                            RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                          76 CCAATCATCCTTTACCACG 94
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                          1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 a \phantom{0}25 c \phantom{0}39 g \phantom{0}18 t \phantom{0} About 1.0 kb after segment 1; chromosome 2q31-q32.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumar,A., Harrison,P.M., Cheung,K.H., Lan,N., Echols,N., Bertone,P., Miller,P., Gerstein,M.B. and Snyder,M. Bertone,P., Miller,P., Gerstein,M.B. and Snyder,M. An integrated approach for finding overlooked genes in yeast An integrated approach for finding overlooked genes in yeast An integrated approach for finding overlooked genes in yeast An integrated approach for finding overlooked genes in yeast Ant. Biotechnol. 20 (1), 58-63 (2002)
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1 (bases 1 to 105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF479941.1 GI:18767077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-FEB-2002) MCD Biology, Yale University, P.O. Box 208103, New Haven, CT 06520-8103, USA
112 bp
Sequence 1 from Patent W00200706
AX343726
                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/protein_id="AAA51999.1"
/db_xref="GI:180411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MLMILWEFNOIARCRVNFTGGDGYKPIILYHVIH" 24 c 20 g 31 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Saccharomyces cerevisiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="YDL025W-A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="YDL025W-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAL79254.1"
/db_xref="GI:18767078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                               52.6%;
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Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                          1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8; Length 105;
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                                                                                                  PAT 01-FEB-2002
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ACCESSION

VERSION

AX343726.1 GI:18491804

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ORIGIN
           BASE COUNT
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCAATNNNNNNNNNCCACG 19
                                                                               Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 199243959-A 4 14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 122)
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic reticulum stress-response regulatory element
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E28800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamberty,M., Bulet,P., Latorse,M.P. and Hoffmann,J. Antimicrobial peptides of the family of defensins, polynucleotides encoding said peptides, transformed vectors and organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhobio (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macrotermitinae; Pseudacanthotermes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera; Orthopteroidea; Dictyoptera; Isoptera; Termitidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudacanthotermes spiniger
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          22
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                                                                          TATA signal
                                                                                         enhancer
                                                                                                                      enhancer
                                                                                                                                                                            HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
                                                                                                          enhancer
                                                                                                                                            Topology: Linear;
                                                                                                                                                          Strandedness: Double;
                                                                                                                                                                                                                             04-MAR-1998 JP 1998052453
                                                                                                                                                                                                                                               14-SEP-1999
                                                                                                                                                                                                                                                          JP 1999243959-A/4
                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
       /organism="Homo sapiens"
/db_xref="taxon:9606"
35 c 48 q 17
                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               GI:13020854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="ACNFQSCWATCOAQHSIYFRRAFCDRSQCKCVFVRG"
17 c 23 g 44 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAD22379.1"
/db_xref="GI:18491805"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pseudacanthotermes spiniger"
/db_xref="taxon:115113"
<1. .111</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%;
52.6%;
                                                                       80. .98
116. .122.
                                                                                                    15. .33
47. .65
                                                                                                                          Location/Qualifiers
  48 g
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Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 bp
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    17 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112;
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REFERENCE
                                                                                    REFERENCE
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                                                                                                                           SOURCE
                                                                                                                                                                                                                   RESULT 30
AF271990/c
                                                                                                                                      KEYWORDS
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                                                                                                                                                                ACCESSION
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                                                                   AUTHORS
                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                           1 CCAATNNNNNNNNCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 52.6%; es 10; Conservation
 Adenoviruses of Subgroup D
Unpublished
2 (bases 1 to 125)
                        Hlusch J.H., Deryckere, F., Windheim, M., Ruzsics, Z., Arnberg, N., Adrian, T. and Burgert, H.G.
E3/49K: A Novel Early Region 3 Protein Specifically Expressed By
                                                                 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
l (bases 1 to 125)
                                                                                                    human adenovirus type 19p
human adenovirus type 19p
                                                                                                                                                                                Human adenovirus type 19p strain 587
                                                                                                                                             AF271990.1 GI:14279590
                                                                                                                                                                     partial sequence.
                                                                                                                                                                                                  AF271990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FI I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC C12N15/09,
(C12N15/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
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PD
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Patent: JP 2001054391-A 4 27-FEB-2001,
HSP RESEARCH INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
(bases 1 to 125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E44205.1 GI:18633458
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                                                                                                                                                                                                                                                                                                                      Conservative
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H5/00, PC C12R1:91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
JP 2001054391-A/4
27-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 52.6%;
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                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                               Score 10; DB 6;
Pred. No. 1.8e+04;
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Pred. No. 1.8e+04;
                                                                                                                                                                                               125 bp
                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    17 t
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                                                                                                                                                                                               DNA
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                                                                                                                                                                           inverted terminal repeat,
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                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                               0;
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BASE COUNT
ORIGIN
Search completed: November 16, 2002, 02:59:16 Job time: 2579 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                                                                      Query Match 52.6%; Score 10; DB 14; Length 125; Best Local Similarity 52.6%; Pred. No. 1.8e+04; Matches 10; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                    1 CCAATNUNUNUNUNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                Ruzsics,Z. and Burgert,H.G.
Direct Submission
Submitted (25-MAY-2000) Dep. of Virology, Gene Center-Max v.
Pettenkofer Inst., Feodor Lynen-Str. 25, Muenchen 81377, Germany
Location/Qualifiers
                                                                                                                                                                                                                              43 a
                                                                                                                                                                                                                   /organism="human adenovirus type 19p"
/strain="587"
/serotype="19p"
/specific_host="Homo sapiens"
/db_xref="taxon:134640"
/1. .-125"
/note="inverted terminal repeat"
/rpt_type=inverted
/rpt_type=inverted
28 g 29 t
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Occeptight (c) 1933 - 2002 Compagen Ltd. Copyright (c) 1933 - 2002 Compagen Ltd. Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search time 277 Seconds Run on: Rovember 15, 2002, 01:16:17; Search 100 Run time Date 1	Mon Nov 18 08:09:24 2002
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10 10 10 10 10

52.6 52.6 52.6 52.6 52.6 52.6 52.6

AAZ25631;

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The present invention specifically claims an element shown by: (A) a sequence having replaced 1-3 bases with the other base(s), which induces competence of endoplasmic reticulum. Also described are: (1) a DNA induces containing the above mentioned element, optionally further containing a ctivity with stress on endoplasmic reticulum of approach: (1) a DNA having DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation.
                                                                                                                                                                                                   Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 10; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                         Endoplasmic reticulum, ER, stress competence; control element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoplasmic reticulum stress competence control element SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ25631 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-0052453
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                                                                                                                                     100.08; Preu. ...
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis; cancer; autoimmune disease;
                                                                                                                                                                    Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
22
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AAS90032
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AAH65636
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                                                                                                                                                                              DB 20;
                                                                                                                                                                1.4e+03
                                                                                                                                             0; Indels
                                                                                                                                                                    Length 19;
                                                                                                                                          0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ovarian anti
DNA encoding novel
Human EST-derived
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C glutamicum codin
                                                                                                                                       Gaps
                                                                                                                                    0,
        RESULT 3
                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                         The present invention specifically claims an element shown by: (A) a CC 19 bb base sequence, CCAATNNNNN NNNNCCACE (ERSE); or (B) a modified base conscription with Stress on endoplasmic reticulum the other base(s), which induces consider transcription inducing activity with stress on endoplasmic reticulum used for stress concentration inducing activity with stress on endoplasmic containing a promoter DNA; and (2) a vector containing a promoter DNA; and (2) a vector containing the promoter DNA; and (2) a vector containing the element can be used for the inhibition of autoimmune diseases and cystic fibrosis by inhibition of can example from the present invention. Azz25637 represent elements used in .
JP11243959-A.
                                                                                                                                                                                                                                                                                                                            Query Match
                          Endoplasmic reticulum; ER; stress competence; control element; inhibition; growth; apoptosis; cancer; autoimmune disease; cystic fibrosis; ds.
                                                                                                                                                                                                                                                                                                      Matches
                                                                  Endoplasmic reticulum stress competence control element SEQ ID NO:6.
                                                                                                                              23-DEC-1999
                                                                                                                                                          AAZ25633;
                                                                                                                                                                    AAZ25633 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                      1 CCAATCGGCGGCCTCCACG 19
                                                                                                                                                                                                                                                             1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                              Local Similarity es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; F1g 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New control element for stress competence of endoplasmic reticulum -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-603708/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HSPK-) HSP KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endoplasmic reticulum, ER, stress competence; control element, inhibition; growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endoplasmic reticulum stress competence control element SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999 (first entry)
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                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                          Conservative
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52.6%;
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                                                                                                                                                                                                                                                                                              Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                         1.4e+03;
9;
                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                0;
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WPI; 1999-603708/52.

(HSPK-) HSP KENKYUSHO KK

04-MAR-1998; 04-MAR-1998; 14-SEP-1999. JP11243959-A. Homo sapiens. Cystic fibrosis; ds

RESULT 2 AAZ25632

AAZ25632 standard; DNA; 19

Db οy

1 CCAATNNNNNNNNNCCACG 19

1 CCAATNNNNNNNNNCCACG 19

Matches Query Match

19;

Conservative

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Similarity

52.6%;

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New control element for stress competence of endoplasmic reticulum useful for inhibition of growth and induction of apoptosis in cancer \frac{1}{2} \left( \frac{1}{2} \right)
                                                     WPI; 1999-603708/52
                                                                                (HSPK-) HSP KENKYUSHO KK
                                                                                                              04-MAR-1998;
                                                                                                                                          04-MAR-1998;
                                                                                                                                                                       14-SEP-1999
                                                                                                                                                                                                 JP11243959-A
                                                                                                                                                                                                                                                                              Endoplasmic reticulum; ER; stress competence; control element.
                                                                                                                                                                                                                                                                                                       Endoplasmic reticulum stress competence control element SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
                                                                                                                                                                                                                               Rattus sp.
                                                                                                                                                                                                                                                            Cystic tibrosis; ds
                                                                                                                                                                                                                                                                           inhibition;
                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                              AAZ25634;
                                                                                                                                                                                                                                                                                                                                                                                                     AAZ25634 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New control element for stress competence of endoplasmic reticulum -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCAATCGGAGGCCTCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for inhibition of growth and induction of apoptosis in
                                                                                                                                                                                                                                                                 growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                              98JP-0052453
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52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                       19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic containing a promoter DNA; and (2) a vector containing the above mentioned element, optionally further optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of
                                                                                                                                                                                                                  Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                           New control element for stress competence of endoplasmic reticulum
                                                                                                                                                                                                                                                         useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                          WPI; 1999-603708/52
                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                        (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cystic fibrosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endoplasmic reticulum stress competence control element SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces competence of endoplasmic reticulum. Also described are: (1) a DNA reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element containing the above mentioned element, optionally further optionally with the DNA. The element can be used for the inhibition of gymptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAR225632 to AAR225657 represent elements used in an aramonia from the present increases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibition; growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ25635 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCAATCGGAGGCCTCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RESULT 6
AAZ25636
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Вр
                                                                Matches
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoantibody formation. AA225632 to AAZ25657 represent elements used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endoplasmic reticulum; ER; stress competence; control element;
inhibition; growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic reticulum stress competence control element SEQ ID NO:9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cystic fibrosis; ds.
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                                                                                                                                                                                                                                               The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing activities are sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP11243959-A
                                                                                                                                                                     containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
                                                                                                                                                                                                                                                                                                                                                                                                                             New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                         sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                 CELIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-603708/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                           an example from the present invention.
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Local Similarity 52.6%;
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                                                                               Local Similarity
                                1 CCAATNUNUNUNUNCCACG 19
 CCAATGGGAGCGCACCACG 19
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                                                                Conservative
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                                                                               52.6%;
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                                                                   0;
                                                                                Score 10; DB 20;
Pred. No. 1.4e+03;
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                                                                   Mismatches
                                                                      9;
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                                                                                                   Length 19;
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                                                                   Indels
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RESULT 7
AAZ25637
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                          The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATINNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element containing the element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic reticulum stress competence control element SEQ ID NO:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cystic fibrosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New control element for stress competence of endoplasmic reticulum useful for inhibition of growth and induction of apoptosis in cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3; 25pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;
         Endoplasmic reticulum: ER; stress competence; control element;
inhibition; growth; apoptosis; cancer; autoimmune disease;
cystic fibrosis; ds.
                                                                                                                                                                  AAZ25538 standard; DNA; 19 BP
                                                                       Endoplasmic reticulum stress competence control element SEQ ID NO:11
                                                                                                                                      AAZ25638;
                                                                                                        23-DEC-1999
                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                        1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                             1 CCAATCGGAAGGAGCCACG 19
                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                         52.6%;
                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                         Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                             1.4e+03;
                                                                                                                                                                                                                                                                                                                                             DB 20;
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       WPI; 1999-603708/52
                              (HSPK-) HSP KENKYUSHO KK
                                                         04-MAR-1998;
                                                                                 04-MAR-1998;
                                                                                                         14-SEP-1999.
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                 cystic fibrosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention specifically claims an element shown by: (A) a sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element containing the reticulum containing the above mentioned element, optionally further optionally with the DNA. The element can be used for the inhibition of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ35637 to ANZ35657 represent elements used in
                                                                                                                                                                                               Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                      Endoplasmic reticulum stress competence control element SEQ ID NO:12.
                                                                                                                                                                                                                                                           23-DEC-1999
                                                                                                                                                                                                                                                                                      AAZ25639;
                                                                                                                                                                                                                                                                                                       AAZ25639 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-603708/52.
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                                                                                                                                                                                                                                                                                                                                                                                           1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                          ibition; growth;
                                                                                                                                                                                                                                                                                                                                                                      1 CCAATCGACGCCGGCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                      98JP-0052453
                                                                               98JP-0052453.
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                                                                                                                                                                                       apoptosis; cancer; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB ZV, Pred. No. 1.4e+03; Wishmatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                      disease;
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RESULT 10
AAZ25640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                             The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA
having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element
                                                                                                                                                             Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                   New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                     WPI; 1999-603708/52
                                                                                                                                                                                                                                                                                                                                        04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1998;
                                                                                                                                                                                                                                                                                                    (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          JP11243959-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cystic fibrosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum; ER; stress competence; control element:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum stress competence control element SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ25640 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ25640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNUNUN NUNUNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        having transcription inducing activity with stress on endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCAATGATGGTCGACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                     98JP-0052453
                                                                                                                                                                                                                                                                                                                                                                     98JP-0052453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4e+03;
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                         An endoplasmic reticulum stress transcription factor (bZIP) and cc capable of regulating transcription inducing activity exhibited by an CC element (ERSE) can be used in a method for controlling expression of CC an endoplasmic reticulum chaperone. The method comprises expressing CC bZIP. The method can be used for expression of a foreign protein by CC positively regulating expression of an endoplasmic reticulum controlling the expression of CC endoperone gene. bZIP is useful for controlling the expression of CC endoplasmic reticulum chaperone either positively or negatively in CC cells and therefore is useful for treatment or prophylaxis of CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases. CC wounds and ulcers, bZIP also maintains the correct conformation of the expression of a foreign protein. This sequence taken from the cypression of a foreign protein (GRP) promoter GRP78 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZZ5632 to AAZZ5657 represent elements used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA28570 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRP78 promoter ERSE1-like sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA28570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription; regulatory element; ERSE; b%IP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; human; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endoplasmic reticulum; stress; ER; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                       New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-387736/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HSPR-) HSP RES INST INC.
                                                                                                                                                                                                                                                                                           Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                            diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                          for treating cancers, arteriosclerosis, cystic fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAATNUNNNNNNCCACG 19
                sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAATGAGGGTCGACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0163112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98JP-0324227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score 10; DB 20;
pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 19;
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RESULT 12
AAA28571
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                                          An endoplasmic reticulum stress transcription factor (bZIP) and ccapable of regulating transcription inducing activity exhibited by an CC capable of regulating transcription inducing activity exhibited by an CC clement (ERSE) can be used in a method for controlling expression of CC an endoplasmic reticulum chaperone. The method comprises expressing CC bZIP. The method can be used for expression of a foreign protein by CC controlling regulating expression of an endoplasmic reticulum consperone either positively or negatively in CC centrolling and therefore is useful for treatment or prophylaxis of centrols and therefore is useful for treatment or prophylaxis of centrols and therefore is useful for treatment or prophylaxis of the endoplasmic reticulum chaperone and thereby increases the capacity of a foreign protein. This sequence taken from the capacity of a foreign protein (GRP) promoter GRP78 contains an ERSE like Compression of a foreign protein (GRP) promoter GRP78 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA28571 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRP78 promoter ERSE1-like sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA28571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-1998;
09-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                  New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haze K. Yoshida H.
                                                                                                                                                                                                                                                                                                   Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-387736/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                     diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCAATNUNNNNNNNCCACG 19
Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCAATCGGCGGCCTCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98JP-0324227
99JP-0163112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    score 10; DB 21;
pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 19;
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Matches

10;

Conservative

0;

ed. No. 1.4

Query Match Best Local Similarity

52.6%;

Score 10; Pred. No.

1.4e+03;

DB 21;

Length 19; ; Indels

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Gaps

0

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20
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; rat; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRP78 promoter ERSE1-like sequence.
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                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HSPR-) HSP RES INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1999;
                                                                                                                                                                                                                                                                                                                   An endoplasmic reticulum stress transcription factor (b2IP) an capable of regulating transcription inducing activity exhibited by an capable of regulating transcription inducing activity exhibited by an endoplasmic reticulum chaperone. The method comprises expressing an endoplasmic reticulum chaperone. The method comprises expressing b2IP. The method can be used for expression of a foreign protein by b2IP. The method can be used for expression of an endoplasmic reticulum positively regulating expression of an endoplasmic reticulum chaperone gene. b2IP is useful for controlling the expression of chaperone gene. b2IP is useful for controlling the expression of
                                                                                                                                                                                           endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the expression of a foreign protein (GRP) promoter GRP78 contains an ERSE lightcose regulating protein (GRP) promoter GRP78 contains an ERSE lightcose regulating protein (GRP) promoter GRP78 contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-387736/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCAATNUNNNNNNNCCACG 19
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                                                                                                                                            Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endoplasmic reticulum stress transcription factor (known as bZIP) controlling expression of endoplasmic reticulum chaperone, useful treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                          Local Similarity
                                   1 CCAATNNNNNNNNCCACG 19
 CCAATCGGAGGCCTCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoshida H, Mori K,
                                                                        10;
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0324227
99JP-0163112
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                                                                                            52.6%;
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                                                                              0;
                                                                                              Score 10;
Pred. No.
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yura T;
                                                                                                    1.4e+03;
                                                                                                                      DB 21; Length 19;
                                                                                                                                                                                                                 contains an ERSE like
                                                                                        Indels
                                                                                        0;
                                                                                        Gaps
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AAA28573
ID AAA2
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                                                                               AAA28574
                                                                                               RESULT 15
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                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prophylaxis: cancer; arteriosclerosis; ischaemia; wound healing;
cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endoplasmic reticulum; stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRP94 promoter ERSE1-like sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                  An endoplasmic reticulum stress transcription factor (bZIP) an capable of regulating transcription inducing activity exhibited by an capable of regulating transcription inducing activity exhibited by an endoplasmic reticulum chaperone. The method comprises expressing an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by bZIP. The method can be used for expression of a foreign protein by chaperone gene. bZIP is useful for controlling the expression of chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in endoplasmic reticulum chaperone either positively or negatively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HSPR-) HSP RES INST INC
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09-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haze K, Yoshida H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases, wounds and ulcers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                  the endoplasmic reticulum chaperone and thereby increases the the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP94 contains an ERSE like glucose regulating protein (GRP) promoter GRP94.
                                                                                                                                                                                                                                                                                    Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                   sequence.
29-AUG-2000
                               AAA28574;
                                                                AAA28574 standard; DNA; 19
                                                                                                                                                                                                                                        Local
                                                                                                                                                 1 CCAATCGCGCGCGCACCACG 19
                                                                                                                                                                                    1 CCAATNUNUNUNUNCCACG 19
                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                         Conservative
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99JP-0163112.
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   (first entry)
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                                                                         ВP
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                                                                                                                                                                                                                                           Score 10; DB 21;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yura T;
                                                                                                                                                                                                                                                                DB 21;
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C capable of regulating transcription inducing activity exhibited by an 2C element (ERES) can be used in a method for controlling expression of 2C an endoplasmic reticulum chaperone. The method comprises expressing 2C chaperone gene. bzIP is useful for expression of a foreign protein by 2C chaperone gene. bzIP is useful for controlling the expression of cendoplasmic reticulum chaperone either positively or negatively in 2C cells and therefore is useful for treatment or prophylaxis of 2C cencers, arteriosclerosis, cystic fibrosis, ischaemic diseases, 2C the endoplasmic reticulum chaperone and thereby increases the 2C cancers arteriosclerosis, cystic fibrosis, ischaemic diseases, 2C the endoplasmic reticulum chaperone and thereby increases the 2C cancers and ulcers bzIP also maintains the correct conformation of 2C cancers and thereby increases the 2C cancers are all the correct conformation of 3C cancers and 12 feeting protein. This sequence taken from the 2C cancers and 12 feeting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                    Endoplasmic reticulum; stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
          prophylaxis; cancer; arteriosclerosis; ischaemia;
                                                                                                                                               GRP94 promoter ERSE3-like sequence.
                                                                                                                                                                                                                29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                       AAA28575 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
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09-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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99JP-0163112.
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52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No. 1.4e+03;
""omatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
wound healing;
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                                                                 Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                 Gallus domesticus
                                                                                                                                                                                                                                                                                GRP94 promoter ERSE3-like sequence.
                                                                                                                                                                                                                                                                                                                                                 29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             AAA28576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of regulating transcription inducing activity exhibited by a element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing positively regulating expression of a foreign protein by chaperone gene bair is useful for controlling the expression of an endoplasmic reticulum endoplasmic reticulum chaperone either positively or negatively in cancers, arterioscalexosis, cystic fibrosis, ischaemic diseases, the endoplasmic reticulum chaperone and therefore is useful for treatment or prophylaxis of wounds and ulcers bzip also maintains the correct conformation of a foreign protein. This sequence taken from the expression of a foreign protein. This sequence taken from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA28576 standard; DNA; 19 BP
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09-JUN-1999;
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Pred. No. 1
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Best Local
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13-NOV-1998;
                                                                                                                                                                                                                                             Calreticulin promoter ERSE3-like sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of
                              12-NOV-1999;
                                                                                                                                                              prophylaxis; cancer; arteriosclerosis; ischaemia; wound healin
cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
                                                                                                                                                                                           Endoplasmic reticulum; stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene, bZIP is useful for controlling the expression of
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                                                            25-MAY-2000
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                                                                                                                    sapiens
                                                                                                                                                   expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSP RES INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 4 A; 9 C; 5 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                           (first entry)
                              99WO-JP06305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-JP06305
                                                                                                                                                     GRP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%;
52.6%;
                                                                                                                                                   glucose regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10; DB 21;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                 protein; promoter; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 19
AAA28578
ID AAA28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by a element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in
                                                                                                                                                                                                                                                                      Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatm prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the calreticulin (CRT) promoter contains an ERSE like sequence.
                            Haze K,
                                                                                       13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                  Calreticulin promoter ERSE3-like sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA28578 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
                                                                                                                                   12-NOV-1999;
                                                                                                                                                                                                W0200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wounds and ulcers. bZIP also maintains the correct conformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-387736/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HSPR-) HSP RES INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-1999;
                                                          (HSPR-) HSP RES INST INC.
                                                                                                                                                                  25-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCAATGATGGTCGACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                           expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshida H,
                            Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 5 A; 6 C; 5 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                       98JP-0324227
99JP-0163112
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                                                                                                                                   99WO-JP06305
                                                                                                                                                                                                                                                         GRP; glucose regulated protein; promoter; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mori K,
                            Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yanagi H,
                            Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yura
                           Yura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Τ;
                            Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by an
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AAA28680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone, gene. bZIP is useful for controlling the expression of
                                           New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum, stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endoplasmic reticulum chaperone either positively or negatively cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, renamic diseases, wounds and ulcers. bZIP also maintains the correct conformation the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the
                                diseases, wounds and ulcers
                                                                                                                                                                                                                         09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                  WO200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA28680 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                        (HSPR-) HSP RES INST INC
                                                                                                                                                                                                                                           13-NOV-1998;
                                                                                                                                                                                                                                                                              12-NOV-1999;
                                                                                                                                                                                                                                                                                                                 25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERSE1 consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calreticulin (CRT) promoter contains an ERSE like sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCAATGAGGGTCGACCACG 19
                                                                                                                      2000-387736/33
                                                                                                                                                                                                                                                                                                                                                                                                                expression; GRP; glucose regulated protein; promoter; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                     Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                         98JP-0324227
99JP-0163112
                                                                                                                                                                                                                                                                              99WO-JP06305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.6%;
                                                                                                                                                     Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 21;
Pred. No. 1.4e+03;
                                                                                                                                                     Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                     Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n
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Claim 1;

Page 130; 157pp; English

Sequence 19 BP; 3 A; 5 C; 1 G;

1 T; 9 other;

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X666666666668XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                 The present invention relates to a method for screening a substance for controlling ORP150 expression. The method comprises examining the expression of a reporter gene product in the presence of a cell strain transformed by a vector. In the vector, the reporter gene is connected downstream of the promotor region of ORP150 gene and a sample to be tested. The method can be used to obtain drug compositions which alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (BRSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by
                                                                      ORP150 expression. The drug composition can be used for the treatment of various diseases e.g. ischaemic diseases, wounds, ulcers, diabetes, neurodegenerative diseases, cancers or autoimmune diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORP150; drug; ischaemic disease; wound; ulcer; diabetes; ERSE; neurodegenerative disease; cancer; autoimmune disease; promoter; ds
                                                                                                                                                                                                                                                                                                                 expression
                                                                                                                                                                                                                                                                                                                                                       Screening a substance for controlling ORP150 expression,
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-610059/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2000; 2000JP-0055384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2000; 2000JP-0055384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2001238699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;
                                                      sequence is an ERSE consensus sequence which was used in an example from
                                                                                                                                                                                                                                                                          Example 3; Page 9; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                    produce drugs for the treatment of diseases associated with ORP150
                                                                                                                                                                                                                                                                                                                                                                                                                                      (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERSE consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI7(0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI70001 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCAATNNNNNNNNCCACG 19
                                   present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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AAF28780
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       express the heterologous gene in a biologically stressed environment. The current invention thus relates to a nucleic acid construct comprising at least two copies of an endoplasmic reticulum stress element (ERSE). The preferred ERSE of the invention is the sequence shown here which corresponds to a glucose responsive protein (grp) 78 gene promoter ERSE.
                                                                                         Targeted gene expression is tool used for gene therapy of diseases and is based on 2 main strategies: (1) targeted entry of a heterologous nucleic acid to a host cell; and (2) specific tissue or cell expression of the heterologous gene. In general, heterologous gene expression has general purpose Murine Leukaemia Virus (MuLV) Long Terminal Repeat (LTR) promoter sequence. Promoters such as these sometimes fail to adequately
  The construct also comprises a heterologous nucleic acid
                                                                                                                                                                                                                                                 A nucleic acid construct comprises a stress-responsive non-coding regulatory sequence useful in treating and detecting cell proliferative disorders, e.g. cancer, or biological stress resulting from glucose
                                                                                                                                                                                                                   Claim 1; Page 83; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                       WPI; 2001-071484/08
                                                                                                                                                                                                                                                                                                                                                                        (UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2000; 2000WO-US17885,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200100791-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; antidiabetic; dermatological; hepatotropic; gene therapy, heterologous gene expression; stress-responsive regulatory sequence; endoplasmic reticulum stress element; ERSE; glucose responsive protein; grp78; promoter; cell proliferative disorder; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes; human; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endoplasmic response stress element motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF28780,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF28780 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      99US-0141505.
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15..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /bound_moiety= "YY1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /bound_moiety= "CBF/NF`Y proteins"
6..14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "GC-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 19;
1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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ACCCCCCXXX PXX PT PT PT XX PXX PXX PT XX P

capable of regulating transcription inducing activity exhibited by an element (ERRE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum

An endoplasmic reticulum stress transcription factor (bZIP)

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AAA28596
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Example 1; Fig 7; 157pp; English.
                                                                                                          New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful
                                              for treating cancers, arteriosclerosis, cystic fibrosis, ischemic diseases, wounds and ulcers
                                                                                                                                                                                                                                                WPI; 2000-387736/33.
                                                                                                                                                                                                                                                                                                                                                                         (HSPR-) HSP RES INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unspecified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          operatively linked to the regulatory sequence, where expression of the heterologous sequence is regulated by the non-coding sequence and where the heterologous sequence encodes a therapeutic agent effective for provided a cell proliferative disorder or for treating a disorder or associated with glucose starvation or a detectable marker. The invention possibly associated with inflammation, for example neoplastic disorders such as lung cancer, colon-rectum cancer, breast cancer, prostate cancer, uranary tract cancer, uterine cancer lymphoma, oral cancer, pancreatic brain cancer and ovarian cancer. The invention is also useful for cancer, colon-human transgenic animals of the invention is also useful for cancer.

Non-human transgenic animals of the invention include vertebrates such as condenses and contents and con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRP78 promoter ERSE1-like sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA28596 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as rodents, non-human primates, sheep, dogs, cows, pigs, amphibians,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression; GRP; glucose regulated protein; promoter; ss
                                                                                                                                                                                                                                                                                                             Yoshida н,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0163112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0324227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99W0-JP06305
                                                                                                                                                                                                                                                                                                         Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                               Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                               Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, cancers arteriosclerosis, cystic fibrosis, ischaemic diseases, cancers and ulcers. bZIP also maintains the correct conformation of wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
Matches
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 5 A; 10 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide adapter/capture probe 191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ00200 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200216649-A2.
                                                                                                            The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in AB000010-AB013409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (AB000010-AB013409) to a target nucleic acid to form a modified target (AB000010-AB013409) to a target nucleic acid to form a modified with (I). nucleic acid and contacting the modified target nucleic acid with (I) the steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target which further comprises detecting the presence of the modified target
                                                                                                                                                                                                                                                                                                                    Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-2000; 2000US-227948P-
29-AUG-2000; 2000US-228854P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-2001; 2001WO-US26519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                   Claim 1; Page 48; 261pp; English.
                                                              Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
                                                                                                 nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CCAATCGGCGGCCTCCACG 23
              Local Similarity
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 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%;
52.6%;
                    52.6%;
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Pred No. 1.5e+03;
       0
                      Pred. No. 1.5e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                        DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.
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           9
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                                        Length 24;
            Indels
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              0;
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              Gaps
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RESULT 25
ABQ04398/c
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 XX EX PX AC
                                                                                                                         ABQ04439
                                                                                                                                     RESULT 26
                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                            25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid nucleic acid adapter nucleic acid with (I). nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target which further comprises detecting the presence of the modified target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Array comprising adapter sequences useful for immobilizing or detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-AUG-2000; 2000US-227948P.
29-AUG-2000; 2000US-228854P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-2001; 2001WO-US26519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 144; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 CCAATATTACGTGACCACG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an oligonucleotide array (I) comprising at least
                                                                                                                                                                                                                                                                                        Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                    nucleic acid.
                                                                                                          ABQ04439 standard; DNA; 24 BP
Oligonucleotide array; adapter sequence; probe; ss.
                         Oligonucleotide adapter/capture probe 4430.
                                                      11-JUN-2002
                                                                                   ABQ04439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              target nucleic acid sequence,
                                                                                                                                                                             23 CCAATATTACGTGACCACG 5
                                                                                                                                                                                                                                                   Loca 1
                                                                                                                                                                                                         1 CCAATUNNUNUNUNCCACG 19
                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-227948P
                                                        (first entry)
                                                                                                                                                                                                                                                      52.6%;
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                          Score 10; u
                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    has different addresses comprising
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                      DB 24;
                                                                                                                                                                                                                                              .5e+03;
les 9;
                                                                                                                                                                                                                                                                        Length 24;
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XXX ACC XXX AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                 Gunderson K;
                                                              (ILLU-) ILLUMINA INC
                                                                                                                    29-AUG-2000;
                                                                                                                                                                                      27-AUG-2001; 2001WO-US26519.
                                                                                                                                              25-AUG-2000;
                                                                                                                                                                                                                                                       28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide array; adapter sequence; probe; ss
                                                                                                                                                                                                                                                                                                             WO200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide adapter/capture probe 10676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ10685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ10685 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). which further comprises detecting the presence of the modified target nucleic acid, which further comprises detecting the presence of the modified target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 144; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-292068/33
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29-AUG-2000; 2000US-228854P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ILLU-) ILLUMINA INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CCAATATTACGTGACCACG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                            2000US-227948P.
2000US-228854P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                             Claim 1; Page 221; 261pp; English.
                                                                                                                                                                           different specific capture probes
                                                                                                                                                                              Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                           WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                           Gunderson K;
                                                                                                                                                                                                                                                                                                  (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                             25-AUG-2000; 2000US-227948P.
29-AUG-2000; 2000US-228854P.
                                                                                                                                                                                                                                                                                                                                                                   27-AUG-2001; 2001WO-US26519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide adapter/capture probe 10717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ10726 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). which further comprises detecting the presence of the modified target nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an oligonucleotide array (1) comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 221; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            different specific capture probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-292068/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 CCAATATTACGTGACCACG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stomach cancer; ureG gene; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; antigen; antigen; toxin; diagnosis; gastritis; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori ureG gene PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1997;
31-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                pcR primers (see AAV45529 and AAV45530) are designed for the PCR amplification of the Helicobacter pylori ureg gene. The invention relates to recombinant DNA (see AAV62460-61) comprising a fusion gen prepared by ligating an antigenic determinant coding gene (e.g. the prepared by ligating an antigenic determinant coding gene (b.g. the prepared by ligating and A2 and B subunit genes of Vibrio cholerae. Also claimed are chimeric proteins (see AAW80599-600) cholerae. Also claimed are chimeric proteins (see AAW80599-600) cholerae. Also claimed are chimeric proteins in preventative and therapeutic vaccines for H. pylori-proteins in preventative and therapeutic vaccines for H. pylori-proteins in preventative and therapeutic vaccines for H. pylori-proteins in diseases such as gastritis, gastric ulcer, duodenal associated diseases such as gastritis, gastric ulcer, duodenal
                                                                                                                                                                                                                                                                                                                                               New chimeric proteins for use against Helicobacter pylori comprising an antigenic protein of H. pylori and Al and B subunits of Vibrio cholerae toxin, preferably produced by recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DAEW-) DAEWOONG PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-568279/48.
                                                                                                                                                                                                                                                                                                         Example 2-15; Page 13; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCAATNUNNNNNNNCCACG 19
                                                                                                           Sequence 25 BP; 7 A; 2 C; 8 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CCAATATTACGTGACCACG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal
                                                                                                                                       ulcer and gastric cancer.
20 CCAATTTTTACCATCCACG 2
                                                                     Local
                         1 CCAATNNNNNNNNCCACG 19
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                                                                      Similarity
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                                                         Conservative
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97KR-0011950.
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Pred. No.
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Job time : 260 secs

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RESULT 30
ABQ12221/c
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Search completed: November 16, 2002, 02:15:58
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                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200216649-A2
                                                                                                                                                                                             The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a 25 different capture probe selected from a group consisting of the sequences different capture probe selected from a group consisting a target given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid modified target (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid. The steps of above method is useful for detecting a target nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 240; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                     different specific capture probes
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                                                                                                                                                       Sequence 25 BP; 4 A; 5 C; 9 G; 7 T; 0 other;
                                                                                                                                                                                     nucleic acid.
                                                                                                                 Local Similarity
                                             24 CCAATATTACGTGACCACG 6
                                                                       1 CCAATNUNNNNNNCCACG 19
                                                                                                     10;
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Pred. No. 1
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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Compugen Ltd
 BH857113 SALK_0768
AA475936 vh25b10. r
BQ756881 EBem09_SQ
BH251489 SALK_0116
BQ099298 ph28h02.y
BH232183 1006166D1
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BI088613
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BI047605
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AV086215
BM195701
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AV963893
AA168302
BM645289
BE002165
AV060848
AV957023
AV388329
AI843919
BE151291
AW121751
BW121751
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BW129683
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AW091115188
BW1902423
AW371351
AW37135
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AA405167
AA073902
BH812753
BH847929
AZ919927
BH895687
BE936056
BF361951
BH753521
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AV289314
BI399749
BI406859
BI059548
BI0742019
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BI0103913
BI0101165
AD74980
AJ1846641
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AZ921866
BF086094
BH583741
AB927925
BH864991
BF094257
AZ720239
BH223259
AI938545
BG950375
AG0264826
AI549504
BH230343
   AA684809
AQ073902 EP(3)3309
BH8073902 EP(3)309
BH807929 SALK_0630
BH809687 3526_1_35
BE93606 QV2-NN004
BH755521 SALK_0292
BH854781 SALK_0886
AZ726948 RPCI-24-1
AV966893 AV963893
AA168802 EM545400 FM2-BN00888
AV967023 AV957023
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BH797242 SALK_0566
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BH864991 SAIK_0972
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BG95034826 Oryza sat
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BH22096 1006105C0
AA405167 ZU51h01.r
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AZ921866 HRCot4D10
BF086094 CM3-GN005
BH583741 BOGXN16TR
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Qy 1 Db 18 RESULT 2	Query Matc Best Local Matches	BASE COUNT	FEATURES SOURCE	JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	LOCUS DEFINITION ACCESSION VERSION KEYWORDS	RESULT 1	C 881 C 882 C 885 C 886 C 886 C 886 C 886
CCAATNNNNNNNNNNCCACG CCAATGAAATTACGCCACG	h Simi 10;	11 2	Salk 1 The Sa 10010 Tel: 8 Fax: 8 Email: This i TDNA. Class:	Arabidopsis Genome Unpublished (2001) Contact: Joseph R.	riate cress. Arabidopsis thalian Bukaryota; Viridip Spermatophyta; Magu Rosidae; eurosids 1 (bases 1 to 43) Alonso, J.M., Leiss , C., Jeske, A., Karr , Zimmerman, J. and A Sequence-Trdexed	113 076821 dopsis nce. 113 113.1		10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 10 52.6
NCCACG 19 GCCACG 36	52.6%; Score 10; DB 17; Larity 52.6%; Pred. No. 1.5e+04; Conservative 0; Mismatches 9;	rganism="Artrain="Colubration="Colubration="Colubration="Colubration="Colubration="ARTrain="Colubration="ARTrain="Colubration="Colubration="ARTrain="Colubration="ARTrain="Colubration="ARTrain="Colubration="Colubration="ARTrain="Colubration="Colubration="Colubration="ARTrain="Colubration	omic Analysis Labora for Biological Stu nes Road, La Jolla, x1752 edu sequence recovered lies within an an	e intered bibliography of insertion mulations sis Genome hed (2001) Joseph R. Ecker	na lantae; Stre lantae; Stre lantae; Stre lonoliophyta; II; Brassica E,T.J., Bara e,T.J., Bara es,M., Kin Ecker,J.R. Lihrary of	43 .44.95.x Arabidop thaliana genomic GI:21707434	ALIGNMENTS	173 12 BF748094 173 17 BH789270 174 9 AV004354 174 13 BJ121753 174 13 BH895513 175 9 AV022317 175 9 AA596238 175 17 BH855839 176 12 BF347368 178 9 AV097435
	Length 43; ; Indels 0; Gaps 0;	abidopsis thaliana" mbia 0" mbia 0" 076821.44.95.x" 076821.44.95.x" 076821.60 haliana TDNA insertion lines" is performed on Arabidopsis thaliana lines contains one or more TDNA insertion resultant fragment for each line was enced to determine the genomic sequence at insertion. Details of the protocols used can http://signal.salk.edu/tdna_protocols.html" 10 g 11 t	itory (SIGnAL) lies CA 92037, USA I from the left border of notated exon of At4g29100.	MUTALTOUS III (1)6	Embryophyta; Tracheophyta; dons; core eudicots; icaceae; Arabidopsis. en,H., Cheuk,R., Gadrinab er,H., Prednis,L., Shinn,P.	<pre>bp DNA linear GSS 08-JUL-2002 sis thaliana TDNA insertion lines clone SALK_076821.44.95.x, DNA</pre>		BE748094 MR2-BN038 BH789270 SALK_0014 AV004354 AV004354 BJ121753 BJ121753 BH895513 3526_1.34 AV022317 AV022317 AA596238 vo30h10.r BH855839 SALK_0844 BF347368 602020656 AI937584 WP81C04 x AV097435 AV097435
RESULT 3 BQ756881 LOCUS DEFINITION	Qy 1 C Db 40 C	BASE COUNT ORIGIN Query Match Best Local Matches 1		FEATURES Source	הקיקור הקידור הקיקור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הקידור הפידור הפידור הפידור הפידור הפידור הפידור הפידור הפידור הפידור הפידור הפידור הפידור הפידור הרדור הרדור הפידור הדרוד ה	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	AA475936 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
BQ756881 79 bp mRNA linear EST 26-JUL-2002 EBem09_SQ005_E15_R embryo, 1 Day germination, no treatment, cv Optic, EBem09 Hordeum vulgare cDNA clone EBem09_SQ005_E15 5', mRNA	CAATNNNNNNNNCCACG 19 + + CAATGGTTTAGCGCCACG 58	19 a ch l Similari 10; Cons	/db_xref="taxon:10000" /db_xref="taxon:10000" /clone_lib="soares_mammary_gland_NbMMG" /clone_lib="soares_mammary_gland" /clone_lib="soares_mammary_gland" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT)		Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:515955 Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 1.	Waterston, R. The WashU-HHMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800	Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 76) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and	AA475936 AA475936 AA475936 76 bp mRNA linear EST 18-JUN-1997 vh25b10.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:876475 5' similar to TR:E196749 E196749 MRNA; EXPRESSED SEQUENCE TAG;, mRNA sequence. AA475936 AA475936.1 GI:2203787 EST. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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EST.
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Contact: Waugh R, Marshall DF

Contact: Waugh R, Marshall DF
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
                                                                 Arabidopsis Genome
Unpublished (2001)
                                                                                                                Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Ga,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"vector: psporT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into psporT1. Derived from embryos dissected from germinating grains (1 day) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
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/dev_stage="1 Day germination"
/lab_host="DH10B"
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/cultivar="Optic"
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Fax: 858 558 6379
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                                                                                                                                                                                      at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center High quality sequence stop: 69.
                                                                                                                                                                                                                                                                                                                                                                The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 20 c 21 g 19 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Columbia
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                                                                                       /organism="Ostertagia ostertagi"
/db_xref="taxon:6317"
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/note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
                       /dev_stage="L3"
/lab_host="DH10B"
                                                                     /clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
                                                                                                                                                                  Location/Qualifiers
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Pred. No. 1.9e+04;
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BH232183/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence submitted separately Plate: 1006166 row: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible ligation site so sequence was trimmed. Post-ligation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                      /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     larvae were collected from 14 day fecal-sphagnum moss cultures of Ostertagia eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                     /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The library was constructed by Claire Murphy and Dr. James McCarter at Washington University. St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PGR based library using a modified protocol from the SMART PCR cDNA Synthesis kit from Clontech. Directionally cloned into the UDC sites of pAMPI. Nematodes were provided by Dr. Louis Gasbarree of the USDA, Beltsville, MD (1998 barreani.barc.usda.gov). Third stage exsheathed the control of the USDA.
                                                                                                                                                                                                                                          /tissue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                 /lab_host="DH10B"
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Very probable ligation site found so sequence was trimmed. Post-ligation sequence submitted separately. Plate: 1006105 row: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize genomic sequences found using engineered RescueMu transposon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: walbot@stanford.edu
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                                                                                                                                    note="organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids DH10B
                                                                                                     cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH1OB cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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LOCUS BF086094 100 bp mRNA linear EST 19-OCT-200 DEFINITION CM3-GN0052-080900-334-c11 GN0052 Homo sapiens cDNA, mRNA sequence
                                                                                  RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson, D.G., Schulze, S.R., Sciara, E.B., Lee, S.A., Bowers, J.E., Nagel, A., Jiang, N., Tibbitts, D.C., Wessler, S.R. and Paterson, A.H. Integration of Cot analysis, DNA cloning, and high-throughput sequencing facilitates genome characterization and gene discovery genome Res. 12 (5), 795-807 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Georgia
Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA
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                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706-583-0160
                                                                                                                                                                                                                                                                                                                                                                                                                                      / vector: pGEM-TA-Easy: A Cot analysis was performed / note="Wector: pGEM-TA-Easy: A Cot analysis was performed for the sorghum genome. Based on the resulting Cot curve, for the sorghum genome. Based on the resulting Cot curve, whighly-repetitive (HR), / moderately-repetitive (MR), / highly-repetitive (HR), / moderately-repetitive (MR), / highly-repetitive (DNA). The three repetition-based DNA sheared genomic DNA. The three repetition-based DNA sheared genomic DNA. The three repetition-based DNA components were cloned into E. coli to produce HRCOt, components were cloned into E. coli to produce HRCOt, and SLCOt genomic libraries. Blotting and MRCOt, and SLCOt genomic libraries. Blotting and sequencing data indicates that each library is sequencing data indicates that each library is representative of the component from which it was derived. Putative ID listings given for sequences are based on putative ID listings given for sequences in the NCBI NT comparison (blastn) with sequences in the NCBI NT Database. Only the primary match is given (all primary E values are < or = 1.00E-5). In no instance does a 'Cot clone' contain the complete sequence of its putative Nr match."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Sorghum bicolor HRCot"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.ludwig.org.br/scripts/gethtml2.pl?t1-&t2=CM3-GN0052-080
900-334-c11&t3=2000-09-08&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
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                                                                                                                    Brassica oleracea.
Brassica oleracea
1 (bases 1 to 101) Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
E., Garcia Correa, R., Verjovski-Almeida, S., Costa, F.F.,
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                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 553 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 57.
                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA is from a doubled haploid provided by Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
/note=Torgan: pooled: Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized NCI-CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
                                                                                                                                                                                           /clone="IMAGE:1541833"
/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                  /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brassica oleracea"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3712"
/clone="BOGXN16"
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52.6%;
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Pred. No. 2.1e+04;
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                               BF094257
                                               RESULT 13
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Db QΥ

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Query Match
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                                                                                                                                             30 CCAATGTGAAGAAGCCACG 12
                                                                                                                                                                                      1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                       Local Similarity
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BF094257 110 bp mrNA linear EST 19-OCT-200CM4-UT0042-050900-568-e11 UT0042 Homo sapiens cDNA, mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH864991 109 bp DNA linear GSS 05-AUG-20
SALK_097225 Arabidopsis thaliana TDNA insertion lines Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH864991.1 GI:22100889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thaliana genomic clone SALK_097225, DNA sequence.
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                           22 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                               directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can the site of insertion.
                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="SALK_097225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                   52.68;
52.68;
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52.6%;
                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                              Score 10;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                    http://signal.salk.edu/tdna_protocols.html"
24 g
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                                                                                                                                                                                                                                              2e+04;
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                        EST 19-OCT-2000
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RESULT 14
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                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                   CCAATTCCCCTACTCCACG 23
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1 (bases 1 to 110)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 110)
                                                                                                                                                                                    AZ720239
AZ720239.1 GI:12461733
                                                                                                                                                                                                                                                AZ720239 110 bp DNA linear GSS 24-JAN-200 RPCI-24-104K1.TV RPCI-24 Mus musculus genomic clone RPCI-24-104K1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=at2=CM4-UT0042-050
900-568-e11at3=2000-09-05&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
    Tsegaye,G.,
                                                                                                                 Mus musculus
                                                                                                                                                                 GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rua
                                                                                                                                                                                                                                    DNA sequence.
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BF094257.1 GI:10899967
                                                                                                                                         house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence start: 12 quality sequence stop: 109 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natl. Acad. Sci. U.S.A. 97
                   Nierman, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue mRNA and cDNA amplification were performed under low stringency conditions."

38 c 23 g 23 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone_lib="UT0042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
    Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
52.6%;
  Krol, M.,
                   Malek,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10; DB
Pred. No. 2.2e
0; Mismatches
Shvartsbeyn, A.,
                        Shatsman, S., Akinret, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2e+04;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                      BH222899.1
GSS.
                  Email: walbot@stanford.edu
Possible ligation site so sequence
sequence submitted separately.
Plate: 1006109 row: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
10; Conserv
Class: transposon-tagged
                                                                                                  Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                     855 California Ave, Palo Alto,
                                                                                                                                                            Stanford University
                                                                                                                                                                             Department of Biological Sciences
                                                                                                                                                                                                  Contact: Walbot V
                                                                                                                                                                                                                      Unpublished (2001
                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0200 Fax: 301 838 0208
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-104KI.TJ
                                                                                                                                                                                                                                         Maize genomic sequences found using
                                                                                                                                                                                                                                                                Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
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/note="Vector: pTARBACl; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBACl; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBACl cloning vector at the
library was cloned in the pTARBACl cloning vector at the
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Pred. No. 2.2e+04;
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RESULT 16
AI938545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sb55b02.y1 Gm-c1018 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1018-4 5' similar to TR:Q38910 Q38910 XYLOGLUCAN
ENDOTRANSGLYCOSYLASE-RELATED PROTEIN. ;, mRNA sequence.
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                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
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                                                                       High quality sequence stop: 1.
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/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                               This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=pM3-EN0004-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                         Seq primer: puc 18 forward
                                                                                                                                                                                     400-001-g04&t3=2000-04-28&t4=1)
                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

33 c 25 g 24 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was prepared using the Stratagene phluescript II XR library construction kit. Complementary DAN was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI XhoI restriction site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from 2-3 week old greenhouse grown plants. The cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1018-4"
/clone_lib="Gm-c1018"
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/dev_stage="2-3 weeks old"
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/db_xref="taxon:9606"
                      /organism="Homo sapiens"
                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-CT0603-040101-611-h01&t3=2001-01-04&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509–010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deollveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20202663
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+55-11-2707001
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/dev_stage="Adult"
                                            ,716 Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                      /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
                                                                                                                                                                                                                                       /dev_stage="Adult"
                                                                                                                                                                                                                                                                /clone_lib="CT0603"
                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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AG024826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-OCT-1999) Akio Miyao, National Institute of Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp, URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020, Fax:81-298-38-7020)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyao, A. and Hirochika, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryze
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                               AI549504 119 bp mRNA linear EST 22-WUI-R-C3-tu-f-02-0-UI.sl UI-R-C3 Rattus norvegicus cDNA clone
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                                        Rattus norvegicus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                              AI549504.1
                                                          Norway rat
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/strain="NCO370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="PCR product directly amplified from rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="T02869T"
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Pred. No. 2.2e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 bp
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                                                                                                                                                                               EST 22-MAR-1999
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                                                         sequence
BH230343
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1006157D12.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
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                         BH230343.1 GI:16833394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonuclectide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail.cDNA Library Preparation: M.B. Soares Lab Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library (UIR-C3) was constructed as follows: PCRamplified cDNA inserts from UIR-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UIR-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the UIR-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:91-806, 1996)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=/vector: pyTyB3-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day embryos, after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process; UI-R-C3, UI-R-C2p, UI-R-C1, UI-R-C1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                   Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
Department of Biological Sciences
                                                                                                                      Walbot, V
                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                Zea mays
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1 (bases 1 to 120)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               855 California Ave, Palo Alto, CA 94304, USA
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RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BgIII, and ligated to form circular plasmids. DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells were transformed and then screened on LB plates with
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pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
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/tissue_type="leaf"
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/db_xref="taxon:4577"
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: transposon-tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                                Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Haterston, R. and Wilson, R. Washu-Merck EST Project 1997
Washu-Merck EST Project 1997
Onpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 123)
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                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                             IMAGE Consortium (info@image.linl.gov) fo
Seg primer: -28m13 rev2 ET from Amersham
                                                                                                       This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650 725 8221
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was 'RescueMu.' and leaf punches, double digested using BamHI extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B and BglII, transformed and then screened on LB plates with
                                                                                                                                     est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; pBlueScript backbone); Modified maize Mu transposon RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
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/db_xref="taxon:4577"
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/dev_stage="adult"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liao,G.-C., Rehm,E.J. and Rubin,G.M.
Insertion site preferences of the P transposable element in prosophila melanogaster
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University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      recognition sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gerry@fruitfly.berkeley.edu
ce recovery method was inverse PCR.
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/lab_host="pH10B (ampicillin resistant)"
/lab_host="pH10B (ampicillin resistant)"
/lab_host="Ovary Vector: pT7T3D (Pharmacia) with a motified polylinker; Site_1: Not I; Site_2: Eco RI; 1st modified polylinker; Site_1: Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand cDNA was primed with a Not II - oligo(dT) primer (strand 
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/clone="IMAGE:741553"
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37 c 27 g
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/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila
/note PCR was performed on these
transposable element insertion. (The generation of these
transposable element insertion. (The generation of these
insertion strains is described in Rorth P. Szabo K. Bailey
insertion strains is described in Rorth P. Szabo K. Bailey
A. Laverty T. Rehm J. Rubin GM. Weigmann K. Milan M. Benes
                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                       /db_xref="taxon:722
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Pred. No. 2.3e+04;
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BH812753/c
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117 CCAATAGTTTATTTCCACG 99
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                                                                                                      Local Similarity
                                        1 CCAATUNUNUNUNCCACG 19
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                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salk Institute Genomic Analysis Laboratory (SIGNAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn, Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SALK_063023 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_063023, DNA sequence.
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                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ecker@salk.edu
                                                                                                                                                                     /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" a 13 c 39 g 43 t
                                                                                                                                                                                                                                                                                                                 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                       /clone="SALK_063023"
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                                                                                               52.6%;
52.6%;
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                                                                                           Score 10; DB 17; Length 124; Pred. No. 2.3e+04;
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AZ919927/c
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Maize genomic sequences found using engineered RescueMu transposon
                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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Az919927.1 GI:13390126
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A Sequence-Indexed Library of Insertion Mutations in the
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.saik.edu/tdna_protocols.html"
a 20 c 35 g 31 t
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Pred. No. 2.3e+04;
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Plate: 3526_1_35_1 row: Class: transposon-tagged
                                                                                                                                        Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
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3526_1_35_1_C06.2EL_x_1 3526
DNA_sequence.
                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                     Reverse complemented post-ligation sequence from source sequence Plate: 3526_1_35_1 row: 27
                                                                              Email: walbot@stanford.edu
                                                                                                        Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                           Contact: Walbot V
                                                                                                                                                                                                                                   Unpubl
                                                                                                                                                                                                                                                                      Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                          GSS
                                                        Possible ligation site of ends cut by 2 different endonucleases
                                                                                                                                                                                                                                            Maize genomic sequences found using engineered RescueMu transposon
                                                                                                                                                                                                                                                                                                                                                                                Zea mays
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/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
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                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV2-NN0054-230
800-333-g09st3=2000-08-23st4=1)
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                                                                                                                                                                                                                                                                Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Ludwig Institute for Cancer Research
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/db_xref="taxon:9606"
                 /organism="Homo sapiens"
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/dev_stage="adult"
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/cultivar="mixed background w23/A188/B73"
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Pred. No. 2.3e+04;
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BF361951
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                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7t1=QV2&t2=QV2-NN0042-
210800-310-d07&t3=2000-08-21&t4=1)
Seq primer: puc 18 forward
tell primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
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/dev_stage="Adult"
                  /note="Organ: nerrous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                        /clone_lib="NN0042"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No. 2.4e+04;
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Search completed: November 16, 2002, 03:32:34 Job time: 1980 secs
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                                                                                                Matches
                                                                                                             Best Local Similarity
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                                                 46 CCAATTCCTGACCACCACG 64
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                                                                                                    Conservative
                                                                                                               52.6%;
52.6%;
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Pred. No. 2.4e+04;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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   Pred. No. is t score greater and is derived
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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  greater than or equal to the score of the result bein derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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19
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149.377 Million cell updates/sec
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Match Length
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Maximum Match 100%
Listing first 90 summaries
  ccaatnnnnnnnnnccacg
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   DB
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   IS-09-974-300-8096

IS-09-978-200-59

IS-09-910-689-59

IS-10-010-742-59

IS-10-010-742-59

IS-10-010-783-590-10136

IS-09-783-590-1013

IS-09-960-352-13155

IS-09-960-352-13155

IS-09-60-353-338-206

IS-09-339-338-206

IS-10-007-805-206

IS-10-033-528-1836

IS-10-033-528-1836

IS-10-033-528-1836

IS-09-234-093B-1836

IS-09-23-876-5857

IS-09-923-876-5857
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-09-969-373-1152
-09-867-701-3962
Sequence 35, Appl
Sequence 1152, Ap
Sequence 3962, Ap
Sequence 59, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 10136, A
Sequence 1013, Ap
Sequence 1013, Ap
Sequence 206, App
Sequence 206, App
Sequence 206, App
Sequence 1836, Ap
Sequence 1836, Ap
Sequence 1837, Ap
Sequence 1837, Ap
Sequence 1838, Ap
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                                                Sequence 246, App Sequence 6179, Ap Sequence 1180, Ap Sequence 1181, Ap Sequence 1451, App Sequence 1451, App Sequence 2907, App Sequence 1113, Ap Sequence 1113, Ap Sequence 1144, Ap Sequence 1144, Ap Sequence 1484, Ap Sequence 1484, Ap Sequence 372, App Sequence 375, App Sequence 4056, Ap Sequence 4115, Ap Sequence 41174, App Sequence 41174, App Sequence 1592, Ap Sequence 11304, Ap Sequence 1592, Ap Sequence 1592, Ap Sequence 1592, Ap Sequence 1592, Ap Sequence 1593, App Sequence 1594, App Se
                                      Sequence
                              Sequence
                              8472,
                             Appl
2, Ap
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ALIGNMENTS

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                                                                                                                           ; TYPE: DNA; ORGANISM: Glycine max US-09-969-373-1152
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; Sequence 1152, Application US/09969373
; Patent No. US20020133852A1
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                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-402-100-35/c
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1152
LENGTH: 100
                                           Matches
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Patent No. US20010019834A1
GENERAL INFORMATION:
APPLICANT: Daewoong Pharmaceutical Co, LTD
APPLICANT: Shin, Sung-Seup
APPLICANT: Yu, Young-Hyo
APPLICANT: Yu, Young-Hyo
APPLICANT: Park, Myung-Hwan
APPLICANT: Jung, Hyung-Jin
TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Heliot
FILE REFERENCE: 0136/06140
                                                                                  Query Match
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Best Local Similarity
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LENGTH: 25
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/760,427 PRIOR FILING DATE: 2001-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/402,100
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: KR 97-11950
EARLIER FILING DATE: 1997-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: KR 97-11951
EARLIER FILING DATE: 1997-03-31
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NAME/KEY: misc_feature
LOCATION: ()..()
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                                                               Local Similarity
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1 CCAATNUNNNNNNNCCACG 19
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                                                          52.6%;
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                                         0;
                                  Score 10; DB 10; L. Pred. No. 3.3e+02;
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Pred. No. 2.4e+02;
0; Mismatches 9;
                                                                            DB 10; Length 100;
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                                    0;
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                                    Gaps
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RESULT 5
US-09-778-320-59/c
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US-09-974-300-8096/c
; Sequence 8096, Application US/09974300
; Patent No. US20020146721A1
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SEQ ID NO 8096
LENGTH: 210
TYPE: DNA
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                                                                                                                                                                 Matches
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: HATLOCKET, SISAN L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
CURRENT FILING DATE: 2001-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3962, Application US/09867701 Patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Aglate, Paul A. APPLICANT: Jones, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                           OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: (1)...(210)
                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bacillus clausii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 123
TYPE: DNA
                                                                             152 CCAATTTCGTCTGTCCACG 134
                                                                                                                                                             Local Similarity 52.6 nes 10; Conservative
                                                                                                                       1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                           52.6%;
52.6%;
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                                                                                                                                                                             Score 10; DB 10;
Pred. No. 3.9e+02;
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                                                                                                                                                             Mismatches
                                                                                                                                                                                                Length 210;
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                                                                                                                                                          0;
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NAME/KEY: misc_feature
LOCATION: (1)...(214)
OTHER INFORMATION: n = A,T,C or G
US-09-778-320-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-910-689-59/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 59
LENGTH: 214
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CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
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APPLICANT:
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                                                                                                                 US-09-910-689-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 59, Application US/09910689
Patent No. US20020081609A1
В
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                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 59
                                                                                                                                                                                                                                                            APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIACNOSIS OF BREAST CANCER FILE REPERBNCE: 210121.491C6
CURRENT PEDILCATION NUMBER: US/09/910,689
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEO ID NOS: 307
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dillon, Davin C. APPLICANT: Day, Craig H. APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                     Query Match
                                                            Matches
                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 34, 120, 153, 159, 171, 179, 184, 194, 197
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                      ENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 CCAATTCTTCATCTCCACG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAATNNNNNNNNNCCACG 19
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 88 CCAATTCTTCATCTCCACG 70
                              1 CCAATNNNNNNNNCCACG 19
                                                                           ocal
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US20010034052A1
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McNeill, Patricia D.
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Mitcham, Jennifer
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                                                                           Similarity
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McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                    Houghton, Raymond
Mitcham, Jennifer
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                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOSITIONS AND METHODS FOR THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raymond L.
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                                                                               52.6%;
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pred. No. 3.9e+02;
                                                                               Score 10; DB 10;
Pred. No. 3.9e+02;
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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                                                                                                 Length 214;
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US-10-010-742-59/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; LOCATION: 34, 120, 153, 159, 171, 179, 184, 194, 197; OTHER INFORMATION: n = A,T,C or G US-10-010-742-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59, Application US/10010742
Patent No. US20020146727Al
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-783-590-10136
Sequence 10136, Application US/09783590
Patent No. US20020110850A1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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CURRENT FILING DATE: 2001-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                             PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 10136
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Hacdong
                                                                                                                                                                                                                                                                  APPLICANT: Rosen, Craig A. APPLICANT: Ruben, Steven M. APPLICANT: Ruben, Steven M. TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/420,856
                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/783,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                   CURRENT FILING DATE:
OTHER INFORMATION: n equals a,t,g, or c
                NAME/KEY: misc feature LOCATION: (3)
                                                                 ORGANISM: Homo sapiens
                                                                                 TYPE: DNA
                                                  FEATURE:
                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 CCAATTCTTCATCTCCACG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                     219
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Zehentner, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Tongtong
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fanger, Gary R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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 Mismatches

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Pred. No. 3.9e+02;
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NAME/KEY: misc feature

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

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; ORGANISM: Homo sapiens US-09-777-564-1013
                                                                                                                                                 SOFTWARE: Fast
SEQ ID NO 1013
LENGTH: 237
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                           US-09-777-564-1013
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                                                                  Matches
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                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                         Sequence 1013, Application US/09777564
Patent No. US20020022591A1
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REPERENCE: 210121.493
                                                                                                                                                                                                                                                                                            APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or c
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18 CCAATTTCAGCCTGCCACG 36
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                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (186)
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                             1 CCAATNNNNNNNNNCCACG 19
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LOCATION: (145)
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                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                    FastSEQ for Window Version 4.0
                                                          Conservative
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                                                                52.6%; Score 10; DB 10; 52.6%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.6%;
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10; DB 10;
Pred. No. 3.9e+02;
Pred. No. 3.9e+02;
                                                                             DB 10; Length 237;
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; APPLICANT: Jiang, Yuqiu; APPLICANT: Dillon, Davi
                                                                                         Sequence 206, Application US/09604287A; Patent No. US20020064872A1
                                                                                 ; GENERAL INFORMATION:
                                                                                                                             US-09-604-287A-206
                                                                                                                                               RESULT 12
                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                   US-09-878-574-6181
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: ENYrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT FILLE REFERENCE: 38-21(15401)B

CURRENT FILLE ADTE: 2001-12-21

CURRENT FILLE JATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEO ID NOS: 15775
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                                      APPLICANT:
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; OTHER INFORMATION: Clone ID: 56-LIB34-004-Q1-E1-F8
US-09-960-352-13155
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6181
LENGTH: 247
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION UNMERR: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 238
TYPE: DNA
OREMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-960-352-13155/c
; Sequence 13155, Application US/09960352
; Pattent NO. US20020137139A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6181, Application US/09878574 Patent No. US20020110548A1
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                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701097950H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                     242 CCAATAACTGTTCGCCACG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APFLICANT: Warren, APFLICANT: Tao, N
                                                                                                                                                                                                                   1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 CCAATATGTTAGATCCACG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 10; Conserv
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                                                                                                                                                                                                                                                          10;
Xu, Jiangchun
Harlocker, Susan L.
                              Mitcham, Jennifer L.
                                             Dillon, Davin C
                                                                                                                                                                                                                                                     Conservative
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Byatt, John C
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Pred. No.
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Pred. No. 4e+02;
                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                             4e+02;
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                                                                                                                                                                                                                                      0;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-604-287A-206
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US-09-339-338-206
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 206
LENGTH: 261
                                                                                                                                                                                                                                                                                                            RESULT 14
US-10-007-805-206
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CURRENT APPLICATION NUMBER: US/09/604,287A

CURRENT FILING DATE: 2000-06-22
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. US20020102602A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 206,
                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                       Sequence 206, Application US/10007805
Patent No. US20020150581A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 2101.21.470C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 315
                                                                                         APPLICANT:
APPLICANT: Durham, Margarita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C10
                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                      APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 261
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                  APPLICANT:
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                                                                                                                                               xu, Jiangchun
Harlocker, Susan L.
Hepler, William T.
                                                                       Fanger, Gary R. Vedvick, Thomas S. McNeill, Patricia D.
                                                                                                                                                                                                     Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                      Dillon, Davin C.
                                                                                                                             Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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52.6%; Pred. No. 4e+02;
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Pred. No. 4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CUBRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 593
SOFTWARE: FASTSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121-547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               sequence 1896, Application US/09294093B
patent No. US20010051335A1
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                                                                                                                   SEQ ID NO 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
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                                                                                                                                                                                                                                                APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REFERENCE: PL-0009 US
                                                                                                                                                                        CURRENT APPLICATION NUMBER: U5/09/294,093B CURRENT FILING DATE: 199-04-16 PRIOR APPLICATION NUMBER: 60/082,567 PRIOR FILING DATE: APRIL 21, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                        NUMBER OF SEQ ID NOS
                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 262
NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. US20010051335A1 700345158H1
                                                           ORGANISM: Zea mays
                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 CCAATTCTTCATCTCCACG 158
                                     FEATURE:
                                                                                              LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 CCAATTCTTCATCTCCACG 162
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                                                                                                                                         PERL Program
                                                                                                                                                                                                                                                                                                                            Lalgudi, Raghunath, V.
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Pred. No. 4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10; DB 12;
Pred. No. 4.1e+02;
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RESULT 18
US-09-783-590-11139/c
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                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                                                                   Sequence 11139, Application US/09783590 Patent No. US20020110850A1
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                                                                                        APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR APPLICATION NUMBER: 095-04-12
                                              PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
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LENGTH: 268
                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                             APPLICANT: Dillon, Patrick J.
                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
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NUMBER OF SEQ ID NOS: 6332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-04-21 PRIOR APPLICATION NUMBER: 60/085,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Incyte ID No. US20020013958A1 700457860H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: 65, 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: 8, 24, 45, 69, 106, 174, 192, 197, 199-200, 206-207, 209, 227, 257,
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 CCAATGGCGCAGGNCCACG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CCAATCCATGGCCTCCACG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                             Haseltine, William A.
                                                                                                                                                                                                                                                           Li, Haodong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.6%;
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57.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 10;
Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                      ; ORGANISM: Homo sapien US-09-867-701-5278
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-867-701-5278/c
                                                                                                                                                              SEQ ID NO 5278
    Best Local Similarity 52.6%; Matches 10; Conservation
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5278, Application US/09867701
Patent No. US20020132237A1
                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEO ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                     APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                          TYPE: DNA
                                                                                                                                        LENGTH: 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 CCAATTCAGTNAAACCACG 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCAATNUNNNNNNNCCACG 19
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57.9%;
          0,
  Score 10; DB 10; Length 274; Pred. No. 4.1e+02; 0; Mismatches 9; Indels
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; OTHER INFORMATION: Clone ID: LIB3028-053-Q1-B1-D5
US-09-878-574-246
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US-09-878-574-246
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SEQ ID NO 3259
LENGTH: 283
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                                                                      Matches
                                                                                        Best
                                                                                                         Query Match
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APPLICANT:
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SEQ ID NO 246
LENGTH: 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
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Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants FILE REFERENCE: 38 2-3 (15401)B CURRENT APPLICATION NUMBER: US/09/878,574 CURRENT FILING DATE: 2001-12-21 PRIOR APPLICATION NUMBER: 05/333,535 PRIOR APPLICATION NUMBER: 09/333,535 PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Byrum, Joseph R. APPLICANT: La Rosa, Thomas J. APPLICANT: Thompson, Michael D.
                                                                                                                                                  NAME/KEY: unsure
LOCATION: 33, 53
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                     NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700379672H1
                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                      Local Similarity
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                                 1 CCAATUNNUNUNUCCACG 19
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CCAATCCCCTTTCCCCACG 22
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                                                                    Conservative
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52.6%;
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52.6%;
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                                                                               Score 10; DB 10;
Pred. No. 4.1e+02;
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Pred. No.
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                                                                  Mismatches
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                                                                                                 Length 283;
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                                                                Indels
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SEQ ID NO 6179
LENGTH: 293
                                                                                                                                                                                                                  SEQ ID NO 8100
LENGTH: 306
TYPE: DNA
ORGANISM: Bacillus clausii
                                     Query Match 52.6%;
Best Local Similarity 52.6%;
Matches 10; Conservative
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Patent No. US20010051335A1
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 00/279,526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOT
FILE REFERENCE: PL-0009 US
                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/082,567 PRIOR FILING DATE: April 21, 1998 NUMBER OF SEQ ID NOS: 6207
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                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(306)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Incyte ID No. US20010051335A1 700383150H1
NAME/KEY: unsure
LOCATION: 250, 255-256
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 CCAATAATCTATTGCCACG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity les 10; Conserv
1 CCAATNUNNNNNNNCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ON: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL PL-0009 US
                                                                                                                                                                                                                                                                                                                                           2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%;
52.6%;
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                               Score 10; DB 10; Le
Pred. No. 4.2e+02;
Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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                                                                        Length 306;
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94 CCAATTTCGTCTGTCCACG 112

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US-09-878-574-1186/c
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-041-Q1-B1-A12
US-09-878-574-1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 25
US-09-938-842A-1451/c
RESULT 26
US-09-728-444-594/c
                                                                          Bb
                                                                                                                                                                                                                                        US-09-938-842A-1451
                                                                                                                                                                                                                                                                         SEQ ID NO 1451
LENGTH: 351
TYPE: DNA
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Byrum, J.
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                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ŠTRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
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                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 339
                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana
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                                                                            143 CCAATCAGAGCCTGCCACG 125
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mes 10; Conserv
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                                                                                                                                                         Conservative
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52.6%; Pred. No. 4.3e+02;
... Mismatches 9;
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Pred. No. 4.3e+02;
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APPLICANT: Sandsrowlcz, Brian
APPLICANT: Sandsrowlcz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020161207Alel Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT APPLICATION NUMBER: US 60/168,360
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 594 SEQ ID NOS: 1206
LENGTH: 358
LENGTH: 358
TYPE: DNA
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, NAME/KEY: misc_feature
; LOCATION: (1)...(358)
; OTHER INFORMATION: n = A,T,C or
US-09-728-444-594
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; ORGANISM: Arabidopsis thaliana US-09-770-791-478
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                                                                             NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 478
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                            APPLICANT: HIJDAN, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thallana
TITLE GFINENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT APPLICATION NUMBER: 0001-01-26
CURRENT APPLICATION NUMBER: 0001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR APPLICATION NUMBER: 60/178,480
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                                                                                                                                            PRIOR FILING DATE: 2000-01-27
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                                                           LENGTH: 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                           Davis, Keith R. Allen, Keith Hoffman, Neil
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Tameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Woessner, Jeffrey P. Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                             Slader,
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Slader, Ted
                                                                                                                                                                                                                                                                                                                                                                                                                     Garcia, Carlos A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matthew,
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52.6%;
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Pred. No. 4.3e+02;
Pred. No. 4.3e+02; Indels
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NAME/KEY: misc_feature

LOCATION: (1)...(365)

OTHER INFORMATION: n = A,T,C or G
US-09-563-817-177
                                                                                                                    ; TYPE: DNA
; ORANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-018-Q1-B1-D9
US-09-878-574-2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-878-574-2907
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US-09-563-817-177
; Sequence 177, Application US/09563817
; Patent No. US20020095031A1
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                                                                                                                                                                                       APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: U5/09/878,574
CURRENT APPLICATION NUMBER: U5/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 2907
LENGTH: 367
                                          Matches
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CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/132,343
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 1008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 177
                                                               Best
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APPLICANT: Nehls, Michael C.
APPLICANT: Sandrowicz, Bria
APPLICANT: Sands, Arthur T.
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TITLE OF INVENTION: No. US20020095031A1el Human Polynucleotides and the TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: LEX-0021-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: homo sapiens
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                                                         Local Similarity
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nes 10; Conserv
1 CCAATNUNNNNNNNCCACG 19
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                                        10;
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                                        Conservative
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52.6%;
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                              Score 10; DB 10, L
Pred. No. 4.4e+02;
"'amatches 9;
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Pred. No. 4.4e+02;
0; Mismatches 9;
                                                                     DB 10; Length 367;
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APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6841
LENGTH: 373
TYPE: DNA
CODONNICM. HOMO SENSION
Search completed: November 16, 2002, 04:29:24 Job time: 49 secs
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US-09-867-701-6841/c
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Matches 10; Conservative
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                                                                                  202 CCAATATAGTAAAACCACG 184
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                                                                                                                      1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                              Score 10; DB IV; Pred. No. 4.4e+02; Pred. No. 4.4e+02;
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